

FIGURE 1

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer HS-1

CGTGGCCATCCTGGGCAACACCCTG

G C GG CT

G

T

HTRHR

CCTGGGCATTGTAGGCAACATCATGGT

HUMRANTES

CATTGGCCTGGTTGGAAACATCCTGGT

HSBLR1A

CCTGGGCGTGATCGGCAACGTCCTGGT

HUMSOMAT

GGTGGGGCTGGTGGGCAACGCCCTGGT

RNU02083

AGTGGGCCTCTTCGGAAACTTCCTGGT

U00442

GGTGGGCTTAGTGGGCAATTCCCTGGT

HUMNMBR

CGTGGGCTTGCTGGGCAACATCATGCT

HSHM4

GGTGACCATCATCGGCAACATCCTGGT

RATAADRE01

CTTTGCCATCGTGGGCAACATCTTGGT

HUMSSTR3X

GGTGGGCCTGCTGGGTAACTCGCTGGT

HUMC5AAR

GGTGGGAGTGCTGGGCAATGCCCTGGT

HUMRDC1A

CATCGGCATGATTGCCAACTCCGTGGT

HUMOPIODRE

CGTGGCGGTGCTCGGCAACCTCGTGGT

RATA2BAR

GCTGGCAGTGGCGGGCAACGTGCTGGT

FIGURE 2

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 3' SIDE PRIMER

Complementary Sequence
to Primer HS-2

TTTGCCATCTGCTGGATGCCCCACAAC

C	C	TTT	C
	G		G
	T		T

HUMSGIR

TTTGCCCTCTGCTGGTTCCCTCTCAAC

HUMBOMB3S

TTTGCCCTCTGCTGGTTGCCAAATCAC

S46950

TTTGCCCTCTGCTGGCTGCCCCCTACAC

MUSGPCR

TTTGCCCTCGTCTGGTGCCCTCTCAAC

S43387

TTTGCCCTTTTATGGATGCCCTACAGG

RATNEURA

TTTGCCATCTGCTGGCTGCCCTATCAC

RATA1ARA

TTTGCCCTCAGCTGGCTGCCGCTGCAT

HUMOPIODRE

TTTGCCATCTGCTGGCTGCCCTATCAC

HUMNEKAR

TTTGCCATCTGCTGGCTGCCCTACCAC

RATADENREC

TTTGCCCTTGTGCTGGCTGCCTTTGTCC

HUMSRI1A

TTTGTCATCTGCTGGATGCCTTTCTAC

S8637154

TTTGCTATCTGCTGGCTGCCCTATCAT

RNCGPCR

TTTGCCGCCTGCTGGATGCCTTTTACC

HUMSSTR4Z

TTTGTGCTCTGCTGGATGCCTTTCTAC

RATGNRHA

TTTGCACTGCTGGTCTGAAGCCAGACAAA

FIGURE 3

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer 3A

CTGACCGCTCTIACIACTGACCGATAC

T T GG GT A C
G

Primer 3B

CTGACCGCTCTIACIACTGACCGATAT

T T GG GT A C
G

L11064	CTCACCATGATGAGCGTGGACCGCTAC
L11065	TTGACCATGATGGAGTGTGACCGCTAC
D16349	CTCTGCACCATGAGCGTGGACCGCTAC
X69676	CTGATGCTCGTGAGTATCGACCGCTAC
M35328	CTTACGGCACTGTCAGCTGACAGGTAC
M73482	CTCACTGCCCTCAGCGCCGACAGGTAC
M73481	CTCACGGCGCTCTCGGCAGACAGATAC
L08893	TTAACAATTCTCAGCGCTGACAGATAC
X62933	ATGACCGCCATCGCCGCTGACAGGTAC
X62934	ATGACAACTGTGGCCTTTGACAGATAC
J05189	ATGACAGCCATTGCAGTGGACAGGTAT
M60786	CTCTGCGCTCTCAGTGTGGACAGGTAC
L04672	CTCACCTGCCTCAGCATTGACCGCTAC
X61496	TTGCTGGCTATCACTGTGGACCGCTAC
X59249	TTGCTGGCCATTGCTGTAGACCGATAC
L09249	CTCACCTGCCTCAGCATTGACCGCTAC
P30731	CTGACAGCTATCGCAGTGGACCGCCAC
M31210	CTCCTCGCCATCGCCATTGAGCGCTAT
U03642	CTCACCGGCCTCAGCTTCGACCGCTAC

FIGURE 4

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer 3C CTCGCCGCTATIAGCATGGACCGITAC
 G CC G T T

Primer 3D CTCGCCGCTATIAGCATGGACCGITAT
 G CC G T T

L32840	ATTACCTGCATGAGTGTCGATAGGTAC
X64052	CTCACGTGTCTCAGCATCGATCGCTAC
M90065	CTCACGTGTCTCAGCATCGATCGCTAC
M91464	CTCACGTGTCTCAGCATTGATCGATAC
M88096	CTGGTAGCCATCTCTCTGGAGAGATAT
M99418	CTCGTGGCCATAGCCCTGGAGCGATAC
L04473	CTCGTGGCCATCGCACTGGAGCGGTAC
M73969	CTGGCCTGCATCAGTGTGGACCGTTAC
X65858	TTGGCCTGCATCAGTGTGGACCGTTAC
S46665	CTGGCTACCATTAGTGCCGACCGTTTC
M60626	ATCGCCCTCATTGCTCTGGACCGCTGT

FIGURE 5

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 3' SIDE PRIMER

Complementary Sequence TTTACCITCTGTTGGICGCCCTACCACATC
to Primer 6A GT TC T T

Complementary Sequence TTCACCITCTGTTGGICGCCCTACCACATC
to Primer 6B GT TC T T

L11064	TTCGTGGTGTGCTGGGCGCCCATCCACATC
L11065	TTCATCATCTGTTGGACCCCATTCACATC
D16349	TTTATCGTCTGCTGGACCCCATCCACATC
X69676	TTTGTGCTGTGTTGGGTGCCTTTCCAGATC
M35328	TTTGCCTTCTGCTGGCTCCCCAACCATGTC
M73482	TTCATCTTCTGTTGGTTTCCAAACCACATC
M73481	TTGCGCTTCTGCTGGCTCCCCAATCATGTC
L08893	TTTGCCCTCTGCTGGTTGCCAAATCACCTC
X62933	TTTGCCATCTGCTGGCTGCCCTACCACCTC
X62934	TTGCGCATCTGCTGGCTGCCCTTCCACATC
J05189	TTTGCCATCTGCTGGCTGCCCTATCACGTG
M60786	TTGCGCCTGTGCTGGTTCCCTCTTCACTTA
L04672	TTTGTCATCTGCTGGCTGCCCTACCACGTG
X61496	TTTGCCGCCTGCTGGATGCCTTTTACCCTC
X59249	TTTGCCTTGTGCTGGCTGCCTTTGTCCATC
L09249	TTTGCCATCTGCTGGCTGCCCTACCACGTG
P30731	TTTGCCCTCTGCTGGTTCCCTCTCAACTGC
M31210	TTCATCGCCTGCTGGGCACCGCTCTTCATC
U03642	TTTGCCCTGTGCTGGATGCCCTACCACCTG

FIGURE 6

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 3' SIDE PRIMER

Complementary Sequence TTTTTCITTTGCTGGITTCCCTACCATG
to Primer 6C : CC T G C T T

L32840	TTCATCATTTGCTGGCTTCCCTTCCATGTT
X64052	TTCTTCTTTTCCTGGGTTCCCCACCAAATA
M90065	TTCTTCTTTTCCTGGGTTCCCCACCAAATA
M91464	TTTTTCTTTTCCTGGATTCCCCACCAAATA
M88096	TTCTTCCTGTGCTGGATGCCCATCTTCAGC
M99418	TTCTTCCTGTGTTGGCTGCCAGTGTACAGC
L04473	TTTTTTCTGTGTTGGTTGCCAGTTTATAGT
M73969	TTCTTGCTTTGCTGGCTGCCCTACAACCTG
X65858	TTCTTGCTTTGCTGGCTGCCCTACAACCTG
S46665	TTCTTTATCTTCTGGCTGCCCTATCAGGTG
M60626	TTTTTTCTCTGCTGGTCCCCATATCAGGTG

L32840
X64052
M90065
M91464
M88096
M99418
L04473
M73969
X65858
S46665
M60626

FIGURE 7

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer T2A

GTCACCAACITGTTTCATCCTCAICCTG

C

AC

GT T

A

HUMGALAREC

ACCACCAACCTGTTTCATCCTCAACCTG

RATADRA1B

CCCACCAACTACTTTATCGTCAACCTG

HUMADRB1

ACCACCAACCTGTTTCATCCTCAACCTG

RABIL8RSB

GTCACCGACGTCTACCTGCTGAACCTG

HUMOPIODRE

GTCACCAACTCCTTCCTCGTGAACCTG

BTSKR

GTGACCAACTACTTCATCGTCAACCTG

HUMSRI2A

ATCACCAACATTTACATCCTCAACCTG

HUMSSTR3Y

GTCACCAACGTCTACATCCTCAACCTG

HUMGARE

GTCACCAACGCCTTCCTCCTCTCACTG

HUMCCKAR

GTCACCAACATCTTCCTCCTCTCCCTG

HUMSHTR

CCCTCCAACCTACCTGATCGTGTCCCTG

HUMD1B

ATGACCAACGTCTTCATCGTGTCTCTG

HUM5HT1E

CCTGCCAACTACCTAATCTGTTCTCTG

HUMD4C

CCCACCAACTCCTTCATCGTGAGCCTG

MMSERO

GCCACCAACTATTTTCCTGATGTCACTT

RATADRA1A

GTCACCAACTATTTTCATCGTGAACCTG

S57565

CTGACCAATTGCTTCATTGTGTCCCTG

FIGURE 8

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence AACCCITCITCTATTGCTTTITCICT
to Primer T7A T T C C C G G

HUMGALAREC	AATCCTATCATTTATGCATTTCTCTCT
RATA1ADREC	AACCCCATCGTCTATGCCTTCCGGATC
PIGA2R	AATCCTCTCTTTTATGGCTTTCTGGGG
RAT5HTRTC	AACCCTATCATCTACCCGCTCTTTATG
S58541	AACCCCATCATTTATGCCTTTAATGCT
HUMGRPR	AACCCCTTTGCCCTCTACCTGCTGAGC
MUSGRPBOM	AACCCCTTTGCTCTTTATCTGCTGAGC
RRVT1AIIR	AACCCTCTGTTCTACGGCTTTCTGGGG
HUMADRB1	AACCCCATCATCTACTGCCGCAGCCCC
HSHM4	AACCCCGTGTGCTATGCTCTGTGCAAC
HUMGARE	AACCCCTGGTCTACTGCTTCATGCAC
RATCCKAR	AACCCCATCATCTATTGCTTCATGAAC
S59749	AATCCCATGCTCTACACCTTCGCTGGC
HUMSST28A	AACCCCGTCCTCTACGGCTTCCTCTCG
RNGPROCR	AACCCCATCCTCTACGGCTTCCTCTCC
MUSSSRI1A	AACCCCATACTCTACGGCTTCCTGTCC
HUMA1AADR	AACCCGCTCATCTACCCCTGTTCCAGC
S66181	AACCCGGTTCTCTACGCCTTCCTGGAC
HUMSSTR3Y	AACCCCATCCTTTATGGCTTCCTCTCC

FIGURE 9

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer TM1-A2 TGITGGTTATIGGIGTTGTIGGIAA
 CC GC C G

MUSBB2R	TGGTGGTGGTGGTGGTGGTGGGCAA
BTSKR	TGGTGCTGGTGGCTGTGATGGGCAA
BOVEETBR	TGTTTCGTGCTGGGCATCATCGGAAA
HUMNEUYREC	TGATCATTCTTGGTGTCTCTGGAAA
MMSUBKREC	TGGTGCTGGTGGCTGTAACAGGCAA
HUMPGE2R	TGTTTCATCTTCGGGGTGGTGGGCAA
HUMPIR	TGTTTCGTGGCCGGTGTGGTGGGCAA
HSU11053	TGTTTCGTGCTGGGCTTGGTGGGCAA
RRMC3RA	TGGTGATCCTGGCTGTGGTGAGGAA
HUMMR	TGGTTATCCTGGCCGTGGTCAGGAA
MUSGRPBOM	TCATCGTGATAGGTCTTATTGGCAA
RATCHOLREC	TCTTTCTGATGAGTGTTGGCGGAAA
RATCCKAR	TATTCCTTCTCAGTGTGCGGGGGAA

FIGURE 10

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence GCCATACCITGGACAGATACCGAT
to Primer TM3-B2 A T A C G A G

HUMCCKR	GCCATCGCACTGGAGCGGTACAG
HUMCCKBGR	GCCATCGCACTGGAGCGGTACAG
MMGMC5R	GCCATTGCGGTGGACAGGTACA
HUMV2R	GCCATGACGCTGGACCGCCACCG
RATNEURA	GCCATTGCAGTGGACAGGTA
DOGGSTRN	GCCATCGCCCTGGAGCGATACAG
RAT5HT5A	GCAATAGCTTTGGACCGCTACTGGT
MUSALP2ADA	GCCATTAGTCTGGACCGCTACTGGT
HUMADORA1X	GCAATTGCTGTGGACCGCTACC
HUMOPIODRE	GCCATCGCGGTGGACAGATACA
MUSGRPBOM	GCACTGTCAGCTGACAGGTACAAA
RATCCKAR	GCCATCTCTCTGGAGAGATATGG
HSTRHREC	GCCTTTACCATTGAGAGGTACATA

FIGURE 11

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer TM3-C2

CATGGCCGTGGAGAGITACITGGC

TT C C T A

HUMNK3R

CATTGCGGTGGACAGGTATATGGC

HSMRNAOXY

CATGTCCCTGGACCGCTGCCTGGC

S68242

CATATCGCTGGAGAGATACGGAGC

CFGPCR4

CATCGCTCTGGACAGGTACTGGGC

MMSUBPREC

TGGCCTTTGACAGATACATGGC

HUMOPIODRE

CATCGCGGTGGACAGATACATGGC

HUMGALAREC

ATGTCCGTGGACCGCTACGTGGC

HSS31G

CATTGCCCTGGACAGGTACTGGGC

HUMARB3A

CCTGGCCGTGGACCGCTACCTGGC

HUMHPR

CATGGCCGTGGAGCGCTGCCTGGC

RATCCKAR

CATCTCTCTGGAGAGATATGGCGC

FIGURE 12

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence TTTGCCITCTGCTGGATCCCCAAC
to Primer TM6-E2 C G C G TT

HUMNEKAR	TTTGCCATCTGCTGGCTGCCCTAC
HUMSUBPRA	TTCGCCATCTGCTGGCTGCCCTTC
RATSKR	TTTGCCATCTGCTGGCTGCCCTAC
MUSGRPBOM	TTTGCCCTTCTGCTGGCTCCCCAAC
HUMOPIODRE	TTTGCCATCTGCTGGCTGCCCTA
HUMA2XXX	TTTGCCCTCTGCTGGCTGCCCT
HUMADRBR	TTCACCTCTGCTGGCTGCCCTTC
CFGPCR8	TTCGCCCCCTCTGTGGCTGCCCT
HUMETSR	TTTGCCCTCTGCTGGCTTCCCCT
MMNPY1CDS	TTCGCCGTCTGCTGGCTGCCCT
HSMRNOXY	TTCATCGTGTGCTGGACGCCTTTC
RATCCKAR	TTCTTCCTGTGCTGGATGCCCATC

FIGURE 13

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer TM2F18

ARYYTIGCIITIGCNGAY

HUMTSHX	AACCTGGCCTTTGCGGAT
HUMNEKAR	AATCTGGCGCTGGCTGAC
HUMFMLP	AACCTGGCCGTGGCTGAC
HUMINTLEU8	AACCTAGCCTTGGCCGAC
HUMAIADR	AACCTGGCCGTGGCCGAC
HUMIL8RA	AACCTGGCCTTGGCCGAC
HSDD2	AGCCTCGCAGTGGCCGAC
HUMANTIR	AATTTAGCACTGGCTGAC
HUMSOMAT	AACCTGGCCGTAGCCGAC
HUMEL4REC	AGCTTGGCTGTGGCTGAT
HSTRHREC	AGCCTGGCAGTAGCTGAT
HSU07882	AACCTGGCCTTAGCCGAT

(R = A or G, Y = C or T, N = A, C, G or T, and
I = Inosine)

FIGURE 14

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence TTYNYNNTNTGYTGGITICCI
to Primer TM6R21

HSBAR	TTCACCCTCTGCTGGCTGCCC
HUMNEKAR	TTTGCCATCTGCTGGCTGCCC
HUMETN1R	TTTGCTCTTTGCTGGTTCCCT
HUMHISH2R	TTCATCATCTGCTGGTTTCCC
HUMA1AADR	TCGTGCTCTGCTGGTTCCCT
HUMIL8RA	TTCCTGCTTTGCTGGCTGCCC
HUMNMBR	TTCATCTTCTGTTGGTTTCCCT
HUMNKIRX	TCGCCATCTGCTGGCTGCCC
HUMSUBPRA	TCGCCATCTGCTGGCTGCCC
HUM5HT1DA	TTTATCATCTGCTGGCTGCCC
HUMPFPR2A	TTCTTCATCTGTTGGTTTCCC
HSDD2	TTCATCATCTGCTGGCTGCCC
HUMNEUYREC	TTTGCAGTCTGCTGGCTCCCT
HUM2XXX	TTTGCCCTCTGCTGGCTGCCC
HUMBK2A	TTCATCATCTGCTGGCTGCCC
HUMFMLPX	TTCTTCATCTGTTGGTTTCCC
HUMSSTR3X	TCGTGCTCTGCTGGATGCCC
HUMCCKR	TTTTTTCTGTGTTGGTTGCCA
HSNEURA	TTTGTGGTCTGCTGGCTGCCC

(Y = C or T, N = A, C, G or T, and I = Inosine)

FIGURE 15

OLIGODEOXYNUCLEOTIDE SEQUENCE FOR 5' SIDE PRIMER

Primer S3A

GCCTGITIAIGATGAGTGTGGAIAGIT
C G C TC CHUMGALAREC
S70057
S67127
S44866
HUMC5AAR
HUMANTIR
HUMBK2A
HSNEURA
HUMGRPR
HUMFSRS
HUMIL8RA
HUMNEKARCCCTGGCCGCGATGTCCGTGGACCGCT
GCCTCGTGGCCATCGCACTGGAGCGGT
ACCTCTGCGCTCTTAGTGTTGACAGGT
GTCTATGTGCTCTGAGTATTGACAGAT
TCCTGGCCACCATCAGCGCCGACCGCT
TACTCACGTGTCTCAGCATTGATCGAT
TCCTGATGCTGGTGAGCATCGACCGCT
ACGTGGCCAGCCTGAGTGTGGAGCGCT
CACTCACGGCGCTCTCGGCAGACAGAT
GCCTGACAGTCATGAGCGTGGACCGCT
TGTTGGCCTGCATCAGTGTGGACCGTT
CCATGACCGCCATTGCTGCCGACAGGT

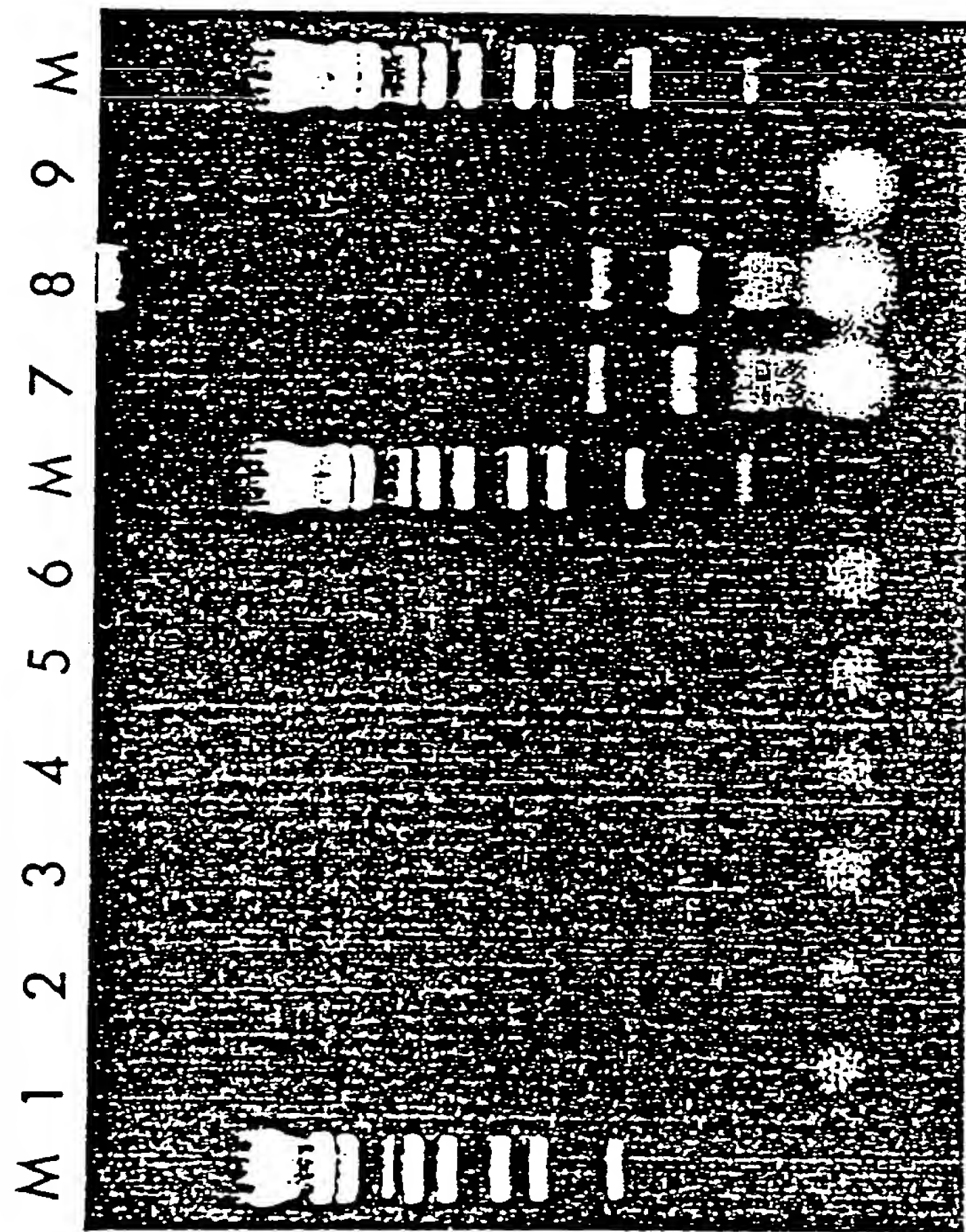
FIGURE 16

COMPLEMENTARY OLIGODEOXYNUCLEOTIDE SEQUENCE TO 3' SIDE PRIMER

Complementary Sequence to Primer S6A	TGGITICCTACCACITATCAICATC T T GG GT
---	--

HUMGALAREC	TGGCTGCCGCACCACATCATCCATCTC
S70057	TGGTTGCCAGTTTATAGTGCCAACACG
S67127	TGGTTCCCTCTTCATTTAAGCCGTATA
S44866	TGGCTTCCCCTTCACCTCAGCAGGATT
HUMC5AAR	TGGTTGCCCTACCAGGTGACGGGGATA
HUMANTIR	TGGATTCCCCACCAAATATTCACTTTT
HUMBK2A	TGGCTGCCCTTCCAGATCAGCACCTTC
HSNEURA	TGGACTCCGTTCTCTATGACTTCTAC
HUMGRPR	TGGCTCCCCAATCATGTCATCTACCTG
HUMFSRS	TGGCTGCCCTTCTTCACCGTCAACATC
HUMIL8RA	TGGCTGCCCTACAACCTGGTCCTGCTG
HUMNEKAR	TGGCTGCCCTACCACCTCTACTTCATC

FIGURE 17



A58-T7-2		10	20	30	40	50
		<u>GTGGCATGGTGGGCAACCCCTGGTCATCTTCGTGATCCTTCGCTACGC</u>				
HUMSOMAT		X:::	:	:	:	:
		GTGGGCTGGTGGGCAACGCCCTGGTCATCTTCGTGATCCTTCGCTACGC				
		285	295	305	315	325
A58-T7-2		60	70	80	90	100
		CAAGATGAAGACGGCTACCAACATCTACCTGCTCAACCTGGCCGTAGCCG				
HUMSOMAT		:	:	:	:	:
		CAAGATGAAGACGGCTACCAACATCTACCTGCTCAACCTGGCCGTAGCCG				
		335	345	355	365	375
A58-T7-2		110	120	130	140	150
		ACGAGCTCTTCATGCTGAGCGTGCCCTTCGTGGCCTCGTCGGCCGCCCTG				
HUMSOMAT		:	:	:	:	:
		ACGAGCTCTTCATGCTGAGCGTGCCCTTCGTGGCCTCGTCGGCCGCCCTG				
		385	395	405	415	425
A58-T7-2		160	170	180	190	200
		CGCCACTGGCCCCTTCGGCTCCGTGCTGTGCCCGCGGTGCTCAGCGTCGA				
HUMSOMAT		:	:	:	:	:
		CGCCACTGGCCCCTTCGGCTCCGTGCTGTGCCCGCGGTGCTCAGCGTCGA				
		435	445	455	465	475
A58-T7-2		210	220	230	240	
		CGGCCACAACATGTTACCACGCGTCTTCTGTCTCACCGTGCTCAGCGT				
HUMSOMAT		:	:	:	:	:
		CGGCCACAACATGTTACCACGCGTCTTCTGTCTCACCGTGCTCAGCGT				
		485	495	505	515	

FIGURE 19

A58-SP6	10	20	30	40	50
	CAGTGTCCACACCCGGCCTGGTCGGCAGTCTTCGTGGTCTACACTTTCCCT				
HUMSOMATA	X:::	:::	:::	:::	:::
	CAGTGGCCACACCCGGCCTGGTCGGCAGTCTTCGTGGTCTACACTTTCCCT				
	706	716	726	736	746
A58-SP6	60	70	80	90	100
	GCTGGGCTTCCTGCTGTCCGTGCTGTCCATGGCCGTGCTACCTGCTCA				
HUMSOMATA	:::	:::	:::	:::	:::
	GCTGGGCTTCCTGCTGTCCGTGCTGTCCATGGCCGTGCTACCTGCTCA				
	756	766	776	786	796
A58-SP6	110	120	130	140	150
	TCGTGGGCAAGATGCGCGCCGTGTCCCTGCGCGCTGGCTGGCAGCAGCGC				
HUMSOMATA	:::	:::	:::	:::	:::
	TCGTGGGCAAGATGCGCGCCGTGTCCCTGCGCGCTGGCTGGCAGCAGCGC				
	806	816	826	836	846
A58-SP6	160	170	180	190	200
	AGGCGCTCGGAGAAGAAATCACCAGGCTGGTGTGAATGGTCTGGTCTGT				
HUMSOMATA	:::	:::	:::	:::	:::
	AGGCGCTCGGAGAAGAAATCACCAGGCTGGTGTGAATGGTCTGGTCTGT				
	856	866	876	886	896
A58-SP6	210	220			
	<u>CTTTGCCCTCTGCTGGTTGCCCTCTCCAC</u>				
HUMSOMATA	:::	:::	:::	:::	X
	CTTTGTGCTCTGCTGGATGCCCTTTCTAC				
	906	916			

	10	20	30	40	50
57-A-2	<u>GTGGGCATGCTGGGCAACCTCCTGGAAGGCAGTCGCCGAGGTGGCCGGTT</u>				
HUMDRD5A	X:::	:	:	:	:
	424	434	444	454	
	60	70	80	90	100
57-A-2	ACTGGCCCTTTGGAGCGTTC T GCGACGTCTGGGTGGCCTTCGACATCATG				
HUMDRD5A	ACTGGCCCTTTGGAGCGTTC T GCGACGTCTGGGTGGCCTTCGACATCATG				
	464	474	484	494	504
	110	120	130	140	150
57-A-2	TGCTCCACTGCCTCCATCCTGAACCTGTGCGTCATCAGCGTGGACCGCTA				
HUMDRD5A	TGCTCCACTGCCTCCATCCTGAACCTGTGCGTCATCAGCGTGGACCGCTA				
	514	524	534	544	554
	160	170	180	190	200
57-A-2	CTGGGCCATCTCCAGGCCCTTCCGCTACAAGCGCAAGATGACTCAGCGCA				
HUMDRD5A	CTGGGCCATCTCCAGGCCCTTCCGCTACAAGCGCAAGATGACTCAGCGCA				
	564	574	584	594	604
	210	220	230	240	250
57-A-2	TGGCCTTGGTTCATGGTTCGGCCTGGCATGGACCTTGTCCATCCTCATCTCC				
HUMDRD5A	TGGCCTTGGTTCATGGTTCGGCCTGGCATGGACCTTGTCCATCCTCATCTCC				
	614	624	634	644	654
	260	270	280	290	300
57-A-2	TTCATTCCGGTCCAGGTCAACTGGGACAGGGACCAGGCGGGCTCTTGGGG				
HUMDRD5A	TTCATTCCGGTCCAGGTCAACTGGGACAGGGACCAGGCGGGCTCTTGGGG				
	664	674	684	694	704
	310				
57-A-2	GGGGCTGGACCTGCCAAA				
HUMDRD5A	GGGGCTGGACCTGCCAAA				
	714	724			

[illegible]

FIGURE 22

5'	9	18	27	36	45	54
GTG GGC ATG GTG GGC AAC GTC CTC CTG GTG ATC GCG GTG CGC CGG						
Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg						
CTG CAC AAC GTG ACG AAC TTC CTC ATC GGC AAC CTG CTG GCC TTG TCC GAC GTG CTC	63	72	81	90	99	108
Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu						
ATG TGC ACC GCC TGC GTG CCG CTC CTC ACG CTG GCC TTC GAG CCA CGC GGC	117	126	135	144	153	162
Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly						
TGG GTG TTC GGC GGC CTG TGC CAC CTG GTC TTC CTG CAG CCG GTC ACC	171	180	189	198	207	216
Trp Val Phe Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr						
GTC TAT GTG TCG GTG TTC ACG CTC ACC ACC ATC GAA GTG GAC CCG TAC GTC GGT	225	234	243	252	261	270
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Glu Val Asp Tyr Val Gly						
GCT GGT GCA CCC GCT GAG GCG GCG CAT 3'	279	288	297			
Ala Gly Ala Pro Ala Glu Ala Gly His						

FIGURE 23

5'	9	18	27	36	45	54
GGC	CTG	CTG	CTG	CTG	CTC	TAC
---	---	ACC	CTC	CTG	ATC	TCT
---	---	TAC	---	---	---	---
Gly	Leu	Thr	Leu	Leu	Ile	Ser
Leu	Leu	Tyr	Pro	Val	Leu	Tyr
Val	Val	---	---	---	---	---
63	72	81	90	99	108	
CGG	GTG	AAG	CTC	CGC	CGG	GTG
---	---	---	---	---	---	---
---	---	---	---	---	---	---
Val	Arg	Val	Lys	Leu	Arg	Pro
Val	Val	Ser	Val	Val	Val	Val
117	126	135	144	153	162	
AGC	CAG	GCC	GAC	TGG	GAC	CGC
---	---	---	---	---	---	---
---	---	---	---	---	---	---
Ser	Gln	Ala	Asp	Trp	Arg	Ala
Val	Val	Val	Val	Val	Val	Val
171	180	189	198	198	198	
GTG	GTG	GTG	GTG	GTG	GTG	GTG
---	---	---	---	---	---	---
---	---	---	---	---	---	---
Val	Val	Val	Val	Val	Val	Val

FIGURE 24

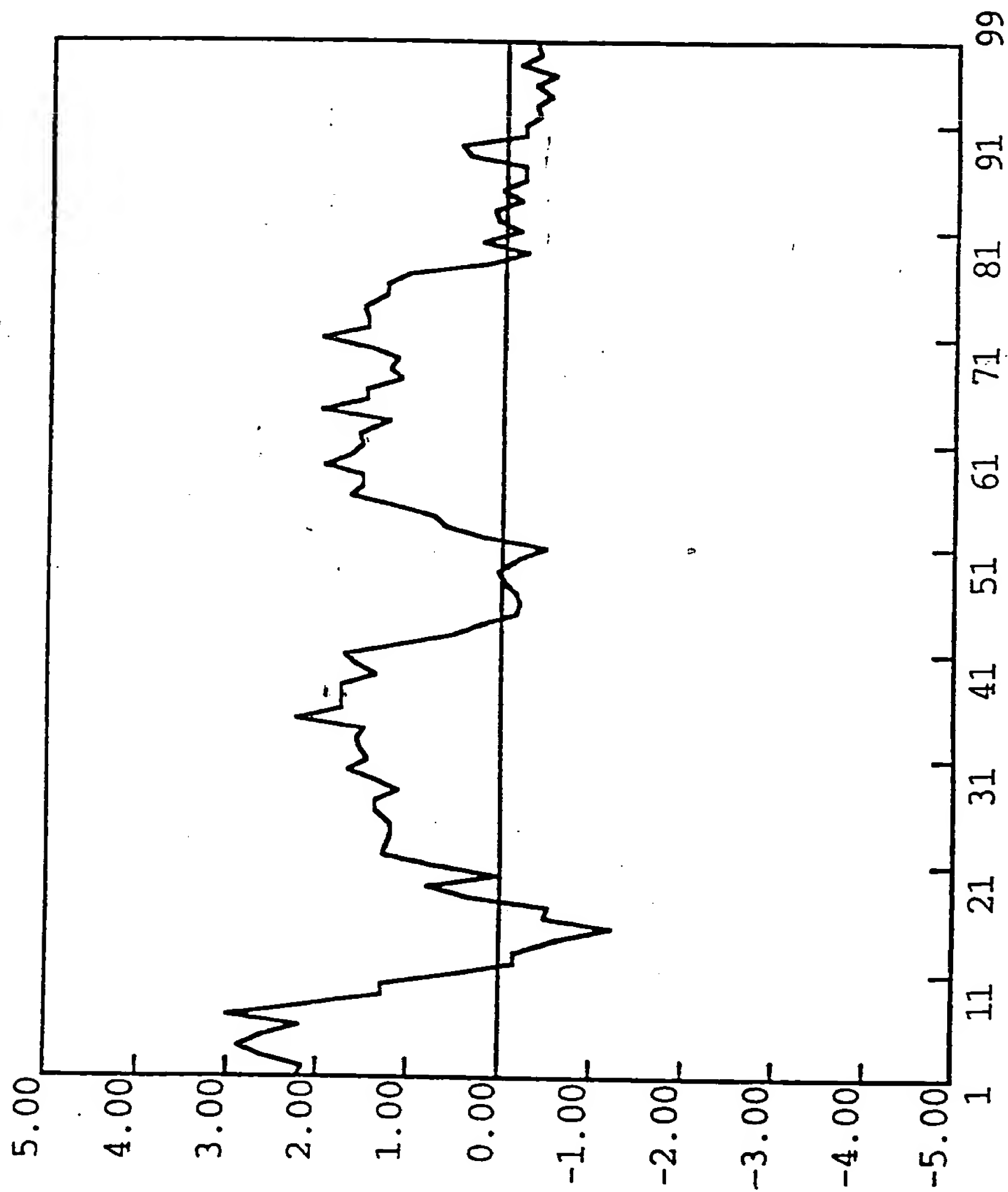


FIGURE 25

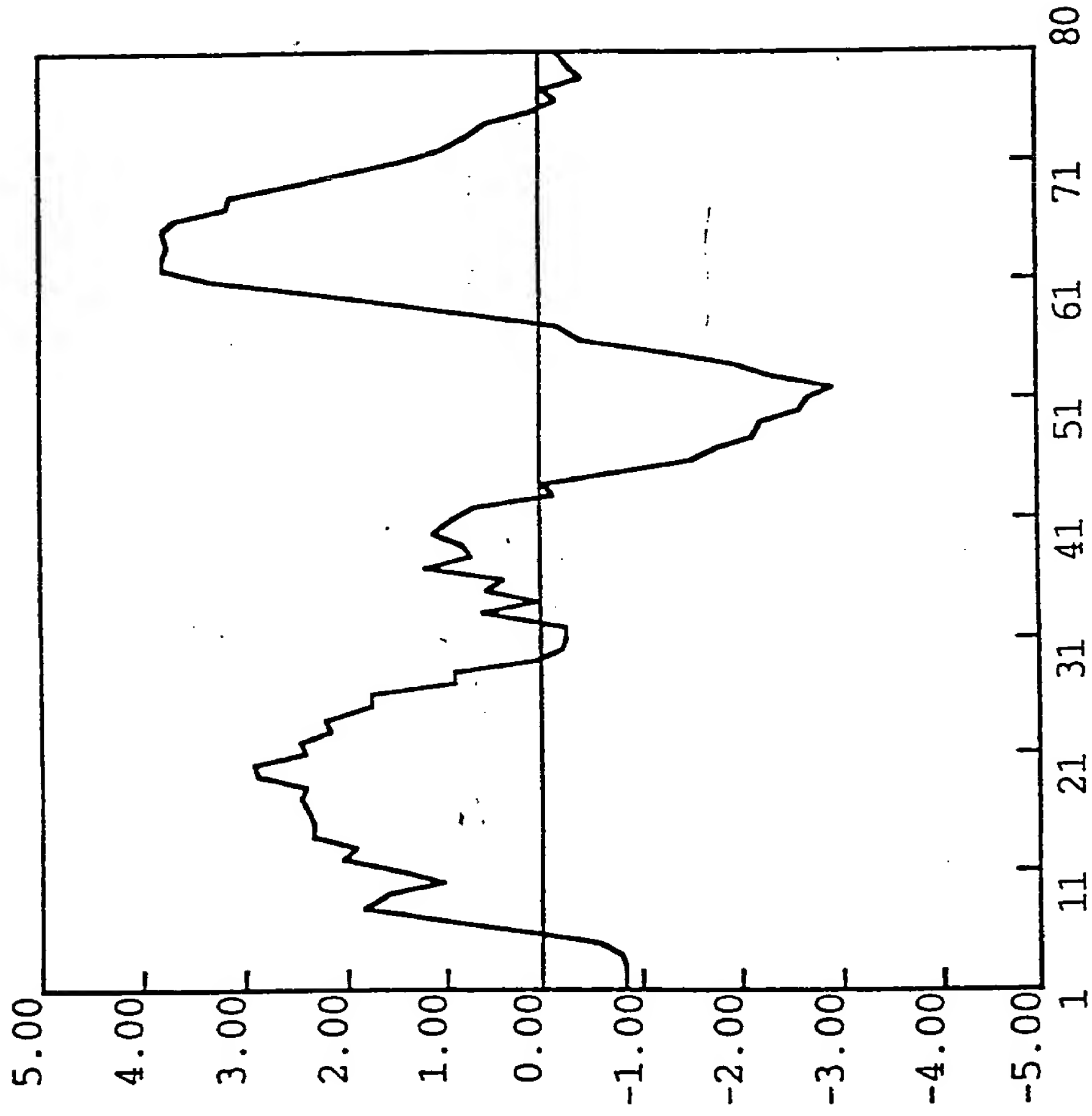


FIGURE 26

		10	20	30	40	50
p19P2	1	VGMVGNVLLV	LVTARVRRLLH	NVTNFLIGNL	ALSDVLMCTA	CVPLTLAYAF
S12863	1	LGVSGNLALI	IIILKQKEMR	NVTNIIIVNL	SFSDLLVAVM	CLPFTFVYTL
		60	70	80	90	100
p19P2	51	EPRGWVFGGG	LCHLVFFLQPV	VTVYVSVFTL	TTIEVDRYVG	AGAPAEAGH
S12863	51	MDH-WVFGET	MCKLNPEVQC	VSI TVSIFSL	VLIIVERHQL	IINPRGWRPN
		110	120	130	140	150
p19P2	101					
S12863	101	NRHAYIGITV	IWVLA VASSL	PFVIYQILTD	EPFQNVSLAA	FKDKYVCFDK
		160	170	180	190	200
p19P2	151	GLLLV	TYLLPLLVIL	LS-----Y	VRSVKLRNPV	VPVCVTQSQA
S12863	151	FPSDSHRLSY	TTLLLVLLQYF	GPLCFIFICY	FKIYIRLKRR	NNMMDKIRDS
		210	220	230	240	250
p19P2	201	DWDRARRRRT	FCLLVVVVVV	FAICWLPPYY		
S12863	201	KYRSSETKRI	NVMLLSIVVA	FAVCWLPLT		

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		657			666		
CTC	TGC	TGG	CTG	CCC	TTC	TTC	3'
---	---	---	---	---	---	---	
Leu	Cys	Trp	Leu	Pro	Phe	Phe	

FIGURE 29

5'	10	19	28	37	46	55												
	GTG	GGC	ATG	CTG	CTG	GCC	CTG	GTC	TGT	CAT	GTC	ATC	TTC	AAG	AAC	CAG	CGA	
	<hr/>																	
				Val	Cys	His	Val	Ile	Phe	Lys	Asn	Gln	Arg					
	64	73	82	91	100	109												
	ATG	CAC	TGG	GCC	ACC	AGC	CTC	TTC	ATC	GTC	AAC	CTG	GCA	GTT	GCC	GAC	ATA	ATG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Met	His	Ser	Ala	Thr	Ser	Leu	Phe	Ile	Val	Asn	Leu	Ala	Val	Ala	Asp	Ile	Met
	118	127	136	145	154	163												
	ATC	ACG	CTG	CTC	AAC	ACC	CCC	TTC	ACT	TTC	GTT	CGC	TTT	GTG	AAC	AGC	ACA	TGG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ile	Thr	Leu	Leu	Asn	Thr	Pro	Phe	Thr	Leu	Val	Arg	Phe	Val	Asn	Ser	Thr	Trp
	172	181	190	199	208	217												
	ATA	TTT	GGG	AAG	GGC	ATG	TGC	CAT	GTC	AGC	CGC	TTT	GCC	CAG	TAC	TGC	TCA	CTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ile	Phe	Gly	Lys	Gly	Met	Cys	His	Val	Ser	Arg	Phe	Ala	Gln	Tyr	Cys	Ser	Leu
	226	235																
	CAC	GTC	TCA	GCA	CTG	ACA	3'											
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	His	Val	Ser	Ala	Leu	Thr												

FIGURE 30

5'	9	18	27	36	45	54
	GAG CCA GCT GAC CTC TTC TGG AAG AAC CTG GAC TTG CCC ACC TTC ATC CTC					
	---	---	---	---	---	---
	Glu Pro Ala Asp Leu Phe Trp Lys Asn Leu Asp Leu Pro Thr Phe Ile Leu Leu					
	63	72	81	90	99	108
	AAC ATC CTG CCC CTC CTC ATC ATC TCT GTG GCC TAC GTT CGT GTG ACC AAG AAA					
	---	---	---	---	---	---
	Asn Ile Leu Pro Leu Leu Ile Ile Ser Val Ala Tyr Val Arg Val Thr Lys Lys					
	117	126	135	144	153	162
	CTG TGG CTG TGT AAT ATG ATT GTC GAT GTG ACC ACA GAG CAG PAC TTT GCC CTG					
	---	---	---	---	---	---
	Leu Trp Leu Cys Asn Met Ile Val Asp Val Thr Thr Glu Gln Tyr Phe Ala Leu					
	171	180	189	198	207	216
	CGG CCC AAA AAG AAG ACC ATC AAG ATG ATG TTG ATG CTG GTG GTA GTC CTC TTT					
	---	---	---	---	---	---
	Arg Pro Lys Lys Lys Lys Thr Thr Ile Lys Met Leu Met Leu Val Val Leu Phe					
	225	234				
	GCC CTC TGC TGG TTG CCT CTC GAC 3'					
	---	---	---	---	---	---
	Ala Leu Cys Trp Leu Pro Leu Asp					

FIGURE 31

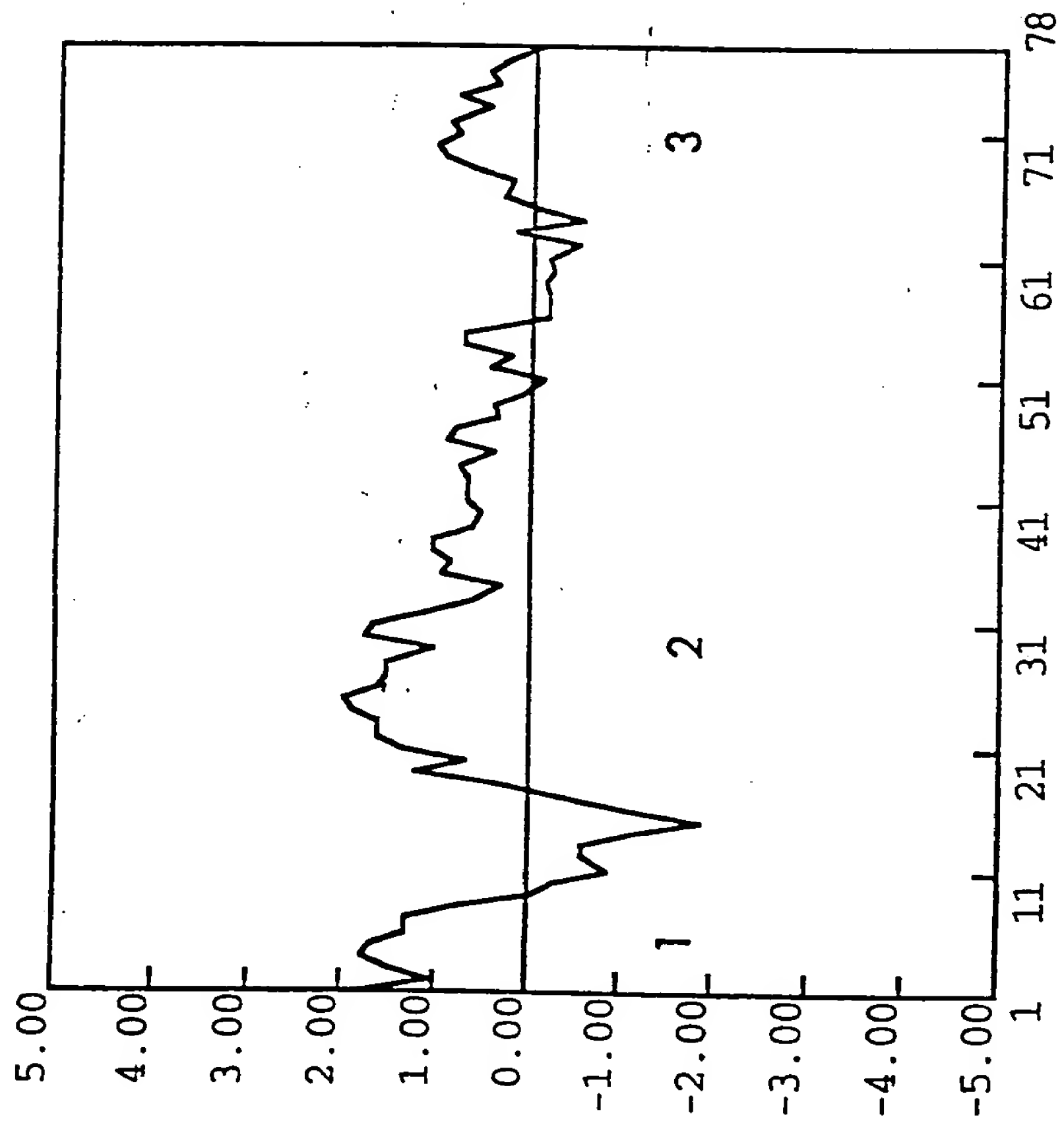
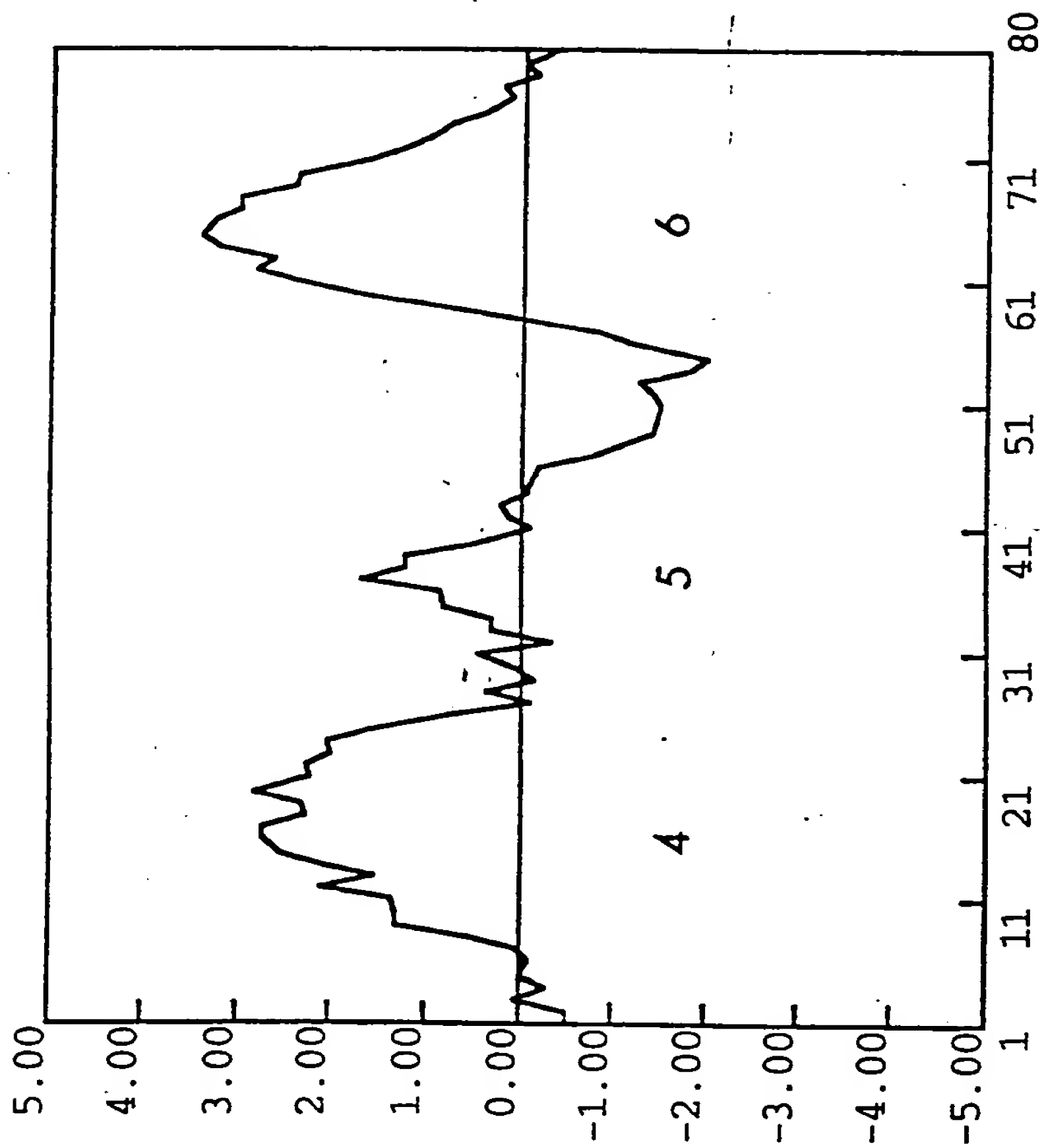


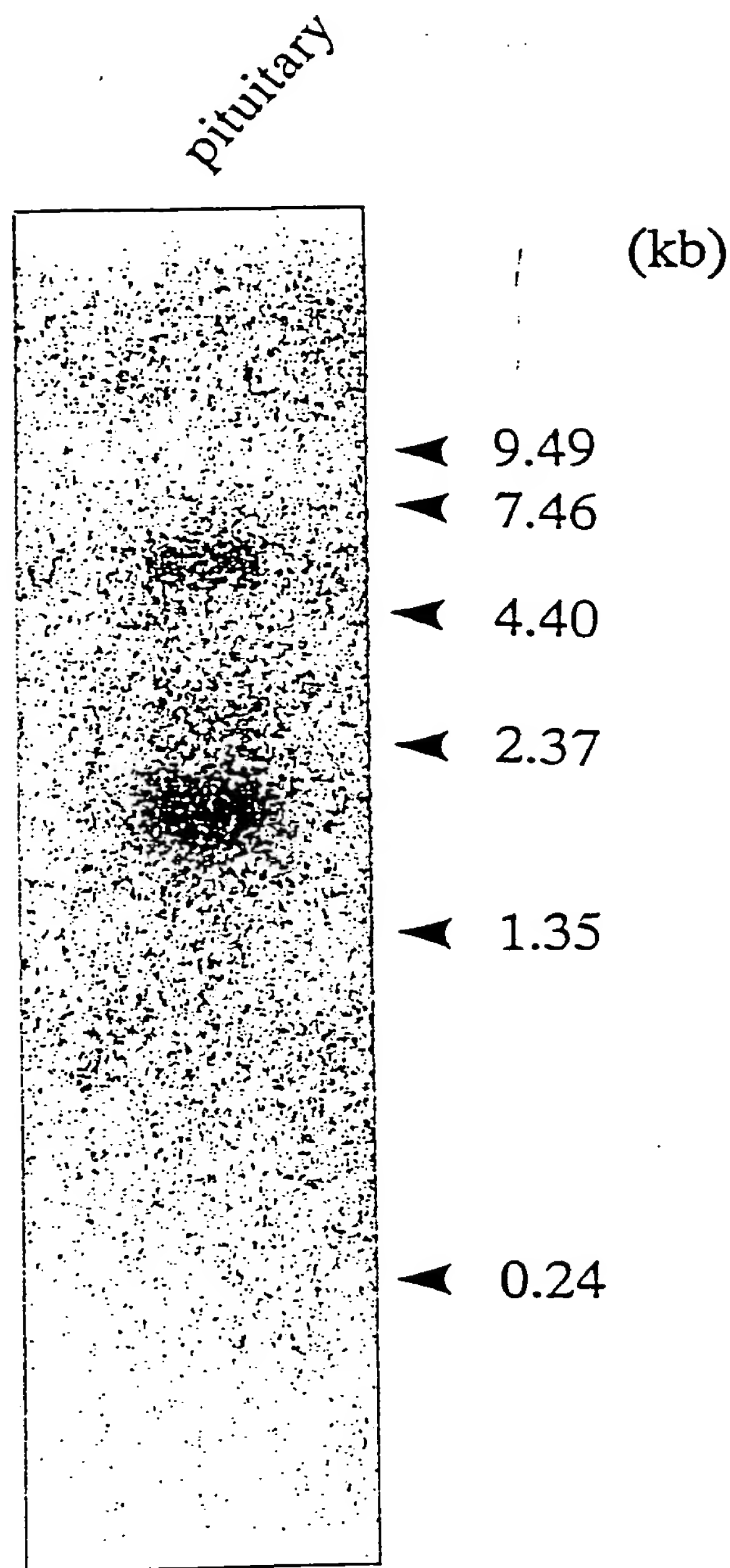
FIGURE 32

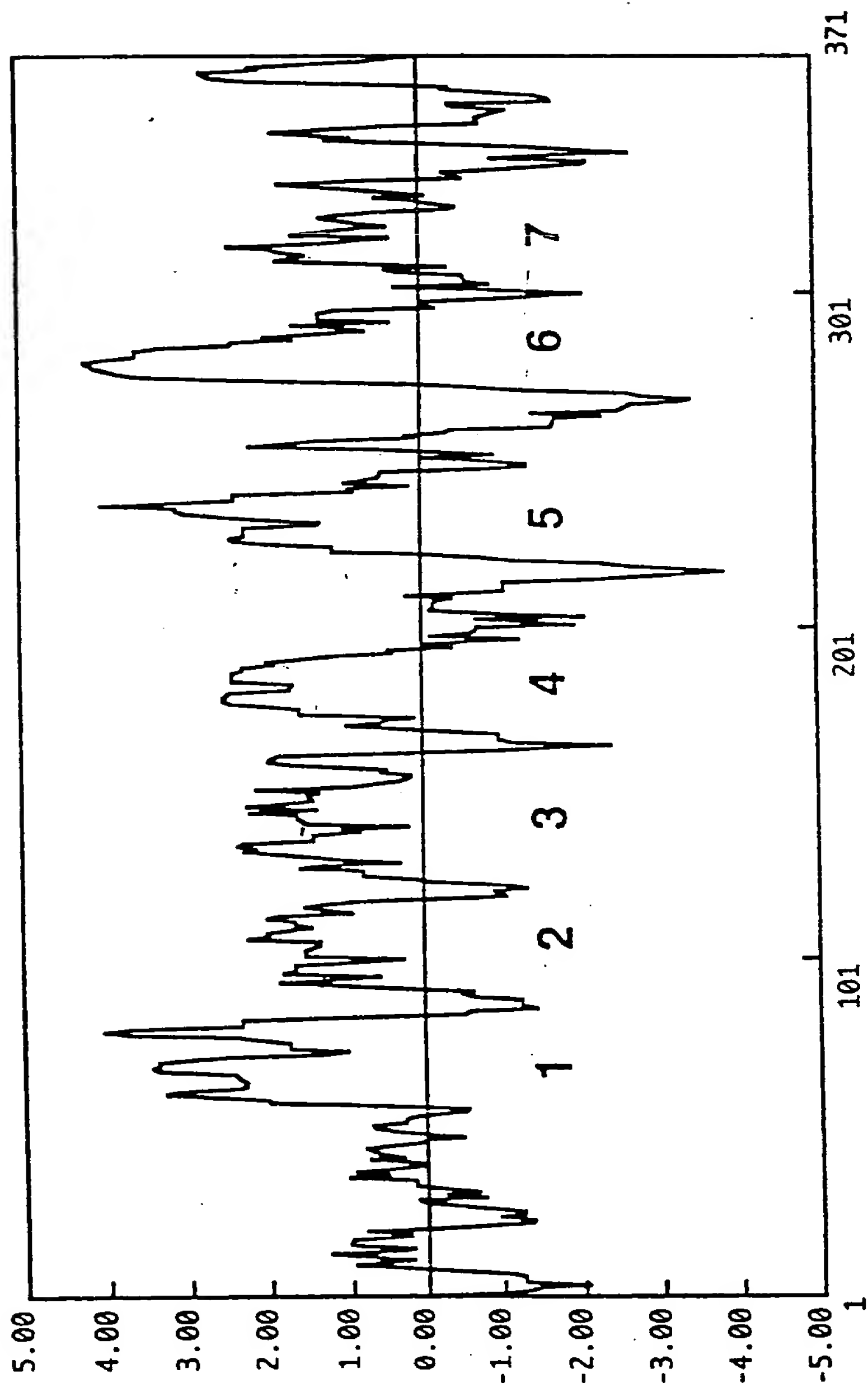


	10	20	30	40	50
p63A2	1 VCHVIFKNQR	MHSATSLFTV	NLAVADIMTT	LLNTPEFTLVR	FVNSTWIFGK
P30731	1 VCHVIFKNQR	MHSATSLFTV	NLAVADIMTT	LLNTPEFTLVR	FVNSTWIFGK
p63A2	51 GMCHVSRFAQ	YCSSLHVSALET	80	90	100
P30731	51 GMCHVSRFAQ	YCSSLHVSALET	LTAIAVDRHQ	VIMHPLKPRI	SITKGVITYLA
p63A2	101	110	120	140	150
P30731	101 VIWVMATFFS	LPHAICQKLF	TFKYSEDIVR	SLCLPDFPEP	ADLEFWKNLDEL
p63A2	151 PTFILINILP	ILLIISVAVVR	180	190	200
P30731	151 ATRILLVLLP	ILFIISVAYAR	VTKKLWLCNM	IGDVTTTEQYF	ALRPKKKKITI
p63A2	201 KMLVLLVVL	210	220	240	250
P30731	201 KMLVLLVVL	210	220	240	250

1	CATCGTCAAGCAGATGAAGATCATCCACGAGGATGGCTACTCCGAGGGCCAGCAGAAATT	60
1		1
61	CTGCCCCCTTCTTCCCGCGAGTGCTTTCCCGCTCTCCAAACCCCACTCCCAGGTGGCCATG	120
1		1
	Met	
121	GCCTCATCGACCACTCGGGGCCCCAGGGTTTCTGACTTATTTTCTGGGCTGCCGCCGGCG	180
1	AlaSerSerThrThrArgGlyProArgValSerAspLeuPheSerGlyLeuProProAla	21
181	GTCACAACTCCCGCCAACCAGAGCGCAGAGGGCTCGGCGGGCAACGGGTGGTGGCTGGC	240
21	ValThrThrProAlaAsnGlnSerAlaGluAlaSerAlaGlyAsnGlySerValAlaGly	41
241	GCGGACGCTCCAGCCGTCACGCCCTTCCAGAGCCTGCAGCTGGTGCATCAGCTGAAGGGG	300
41	AlaAspAlaProAlaValThrProPheGlnSerLeuGlnLeuValHisGlnLeuLysGly	61
301	CTGATCGTGCTGCTCTACAGCGTCGTGGTGGTGGTGGGCTGGTGGGCAACTGCCTGCTG	360
61	LeuIleValLeuLeuTyrSerValValValValValGlyLeuValGlyAsnCysLeuLeu	81
361	GTGCTGGTGATCGCGCGGGTGCGCGGGCTGCACAACGTGACGAACTTCTTCATCGGCAAC	420
81	ValLeuValIleAlaArgValArgArgLeuHisAsnValThrAsnPheLeuIleGlyAsn	101
421	CTGGCCTTGTCGACGTGCTCATGTGCACCGCCTGCGTGCCGCTCACGCTGGCCTATGCC	480
101	LeuAlaLeuSerAspValLeuMetCysThrAlaCysValProLeuThrLeuAlaTyrAla	121
481	TCGAGCCACGCGGCTGGGTGTTCCGCGGCGGGCCTGTGCCACCTGGTCTTCTTCCTGCAG	540
121	PheGluProArgGlyTrpValPheGlyGlyGlyLeuCysHisLeuValPhePheLeuGln	141
541	CCGGTCACCGTCTATGTGTGGTGTTCACGCTCACCACCATCGCAGTGGACCGCTACGTC	600
141	ProValThrValTyrValSerValPheThrLeuThrThrIleAlaValAspArgTyrVal	161
601	GTGCTGGTGCACCCGCTGAGGCGGCGCATCTCGCTGCGCCTCAGCGCCTACGCTGTGCTG	660
161	ValLeuValHisProLeuArgArgArgIleSerLeuArgLeuSerAlaTyrAlaValLeu	181
661	GCCATCTGGGCGCTGTCCGCGGTGCTGGCGCTGCGCGCGCGCGTGCACACCTATCACGTG	720
181	AlaIleTrpAlaLeuSerAlaValLeuAlaLeuProAlaAlaValHisThrTyrHisVal	201
721	GAGCTCAAGCCGACGACGTGCGCCTCTGCGAGGAGTTCTGGGGCTCCAGGAGCGCCAG	780
201	GluLeuLysProHisAspValArgLeuCysGluGluPheTrpGlySerGlnGluArgGln	221
781	CGCCAGCTCTACGCCTGGGGGCTGCTGCTGGTCACCTACCTGCTCCCTCTGCTGGTCATC	840
221	ArgGlnLeuTyrAlaTrpGlyLeuLeuLeuValThrTyrLeuLeuProLeuLeuValIle	241
841	CTCCTGTCTTACGTCCGGGTGTCAGTGAAGCTCCGCAACCGCGTGGTGCCGGGCTGCGTG	900
241	LeuLeuSerTyrValArgValSerValLysLeuArgAsnArgValValProGlyCysVal	261
901	ACCCAGAGCCAGGCCGACTGGGACCGCGCTCGGCGCGCGGCGCACCTTCTGCTTGCTGGTG	960
261	ThrGlnSerGlnAlaAspTrpAspArgAlaArgArgArgThrPheCysLeuLeuVal	281
961	GTGGTGGTGGTGGTGGTTCGCCGTCTGCTGGCTGCCGCTGCACGTCTTCAACCTGCTGCGG	1020
281	ValValValValValPheAlaValCysTrpLeuProLeuHisValPheAsnLeuLeuArg	301
1021	GACCTCGACCCCCACGCCATCGACCTTACGCCTTTGGGCTGGTGCAGCTGCTCTGCCAC	1080
301	AspLeuAspProHisAlaIleAspProTyrAlaPheGlyLeuValGlnLeuLeuCysHis	321
1081	TGGCTCGCCATGAGTTCCGGCCTGCTACAACCCCTTCATCTACGCCTGGCTGCACGACAGC	1140
321	TrpLeuAlaMetSerSerAlaCysTyrAsnProPheIleTyrAlaTrpLeuHisAspSer	341
1141	TTCCGCGAGGAGCTGCGCAAACCTGTTGGTGGCTTGGCCCCGCAAGATAGCCCCCATGGC	1200
341	PheArgGluGluLeuArgLysLeuLeuValAlaTrpProArgLysIleAlaProHisGly	361
1201	CAGAATATGACCGTCAGCGTGGTCATCTGATGCCACTTAGCCAGGCCTTGGTCAAGGAGC	1260
361	GlnAsnMetThrValSerValValIle***	371
1261	TCCACTTCAACTGGCCTCCTAGGGCACCCTCGAGGTCAATCTGGTGGCTTATTCTCAGCA	1320
371		371
1321	CCAGAGCTAGC	1331
371		371

FIGURE 35



[illegible]

[illegible]

FIGURE 38

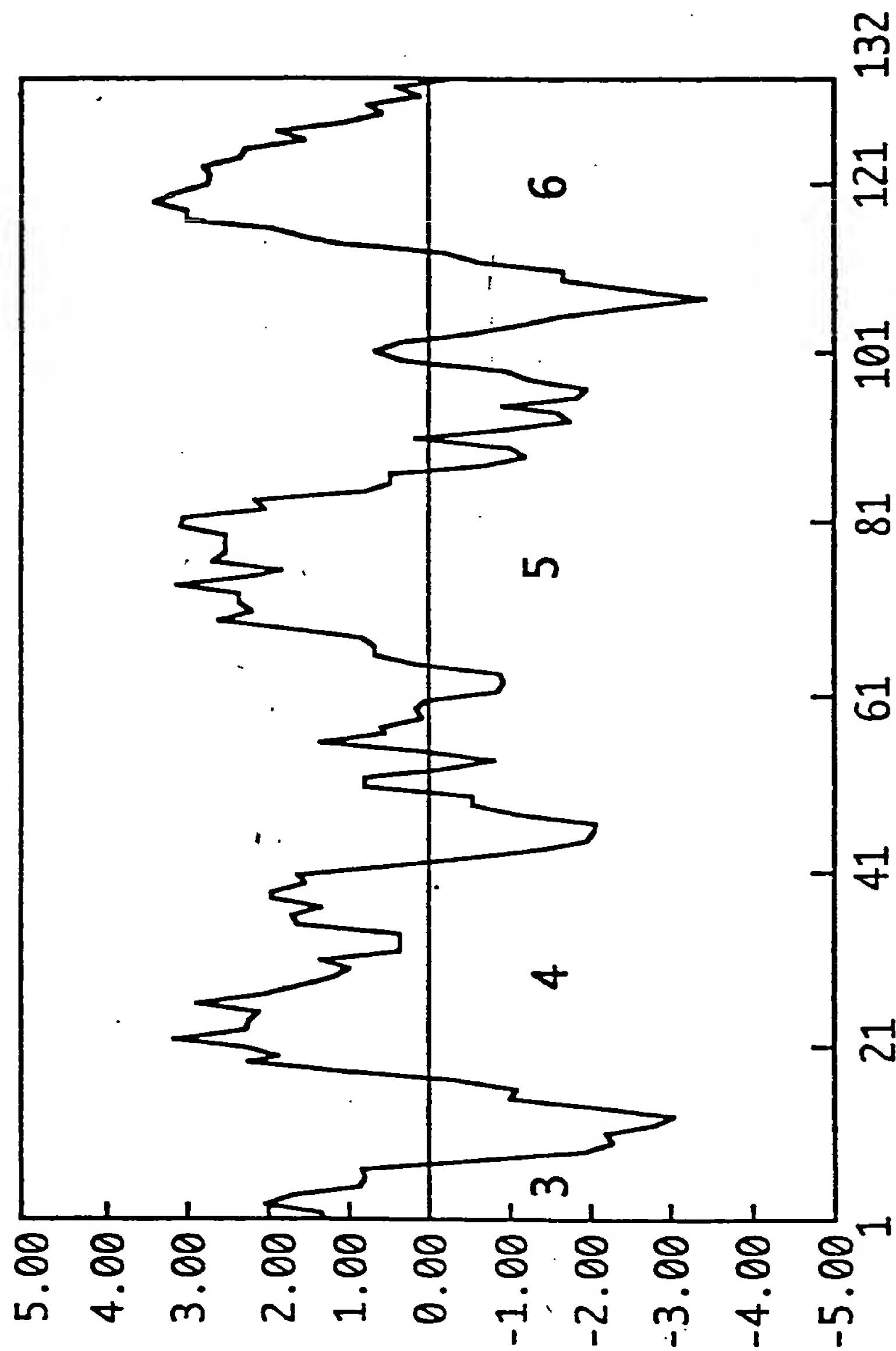


FIGURE 39

p3H2-17	1	10	20	30	40	50	
p34996	1	VGLVGNILAS	WHKRGGRRAA	WVVCGVVWLA	VTAQCCLPTAV	FAATGIGRN-	50
A46226	1	RYTGAVVHPLK	SLGRLKKKNA	VYVSSLVWAL	VVAVIAPILF	YSGTGVRRN-	50
JN0605	1	RYLAVVHPTR	SARWRTAPVA	RTVSAAVWVA	SAVVVLPVVV	F--SGVPRG-	50
S28787	1	RYVAVVHPLR	AATYRRPSVA	KLINLGVWLA	SLLVTLPIAI	FADTRPARGG	50
	1	RYLAIVHATN	SQKPRKLLAE	KVVYVGVWLP	AVLLTIIDLI	FADIKEVDE-	50
p3H2-17	51	RTV-CYDL--	SRPILSTRYL	PYGMALTVIG	FLPFIALLA	CYCRMARRLC	100
p34996	51	KTITCYDT--	TAD EYLRSYF	VYSMCTTVFM	FCIPFIVILG	CYGLIVKALI	100
A46226	51	MST-CHMQWP	EPAAAWRAGE	I IY--TAAALG	FFGPLLVICL	CYLLIVVKVR	100
JN0605	51	QAVACNLQWP	HPAWSAVFVV	YTF---L LG	FLPVLAIIGL	CYLLIVGKMR	100
S28787	51	RYI-CDRF--	YPSDLWL VVE	QFQ--HIVVG	LLPGIVILS	CYCIISKLS	100
p3H2-17	101	RQDGP A-GPV	AQE-RRS--K	AARMVAVVAA	VFALCWLPLY	150
p34996	101	YKDL DN-SPL	---RR---K	SIYLVITVLT	VFAVSYPFH	150
A46226	101	SAGR RVWAPS	CRRRRSERR	VTRMVAVVAA	LFVLCWMPFY	150
JN0605	101	AVALLRA---G	WQRRRSEKK	ITRLVLMVVV	VFVLCWMPFY	150
S28787	101	HSKG-----	YQKR-----K	ALKTIVILIL	TEFACWLPYY	150

FIGURE 40

5'	GTG	GCC	CTG	GTG	GCC	AAC	TTC	CTG	GCC	GCG	ATG	TCT	GTG	GAT	CGC	TAC	GTG	GCC
	Val	Gly	Leu	Val	Gly	Asn	Phe	Leu	Ala	Ala	Met	Ser	Val	Asp	Arg	Tyr	Val	Ala
	ATT	GTG	CAC	TCG	CGG	CGC	TCC	TCC	TCC	CTC	AGG	GTG	TCC	CGC	AAC	GCA	CTG	CTG
	Ile	Val	His	Ser	Arg	Arg	Ser	Ser	Ser	Leu	Arg	Val	Ser	Arg	Asn	Ala	Leu	Leu
	GGC	GTG	GGC	TTC	ATC	TGG	GCG	CTG	TCC	ATC	GCC	ATG	GCC	TCG	CCG	GTG	GCC	TAC
	Gly	Val	Gly	Phe	Ile	Trp	Ala	Leu	Ser	Ile	Ala	Met	Ala	Ser	Pro	Val	Ala	Tyr
	CAC	CAG	CGT	CTT	TTC	CAT	CGG	GAC	AGC	AAC	CAG	ACC	TTC	TGC	TGG	GAG	CAG	TGG
	His	Gln	Arg	Leu	Phe	His	Arg	Asp	Ser	Asn	Gln	Thr	Phe	Cys	Trp	Glu	Gln	Trp
	CCC	AAC	AAG	CTC	CAC	AAG	AAG	GCT	TAC	GTG	GTG	TGC	ACT	TTC	GTC	TTT	GGG	TAC
	Pro	Asn	Lys	Leu	His	Lys	Lys	Ala	Tyr	Val	Val	Cys	Thr	Phe	Val	Phe	Gly	Tyr
	CTT	CTG	CCC	TCA	CTG	CTC	ATC	TGC	TTT	TGC	TAT	GCC	AAG	GTC	CTT	AAT	CAT	CTG
	Leu	Leu	Pro	Leu	Leu	Leu	Ile	Cys	Phe	Cys	Tyr	Ala	Lys	Val	Leu	Asn	His	Leu
	CAT	AAA	AAG	CTG	AAA	AAC	ATG	TCA	AAA	AAG	TCT	GAA	GCA	TCC	AAG	AAA	AAG	ACT
	His	Lys	Lys	Leu	Lys	Asn	Met	Ser	Lys	Lys	Ser	Glu	Ala	Ser	Lys	Lys	Lys	Thr
	GCA	CAG	ACC	GTC	CTG	GTG	GTC	GTT	GTA	GTA	TTT	GCC	CTC	TGC	TGG	CTG	CCT	TTC
	Ala	Gln	Thr	Val	Leu	Val	Val	Val	Val	Val	Phe	Ala	Leu	Cys	Trp	Leu	Pro	Phe

TAC 3'

Tyr

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FIGURE 41

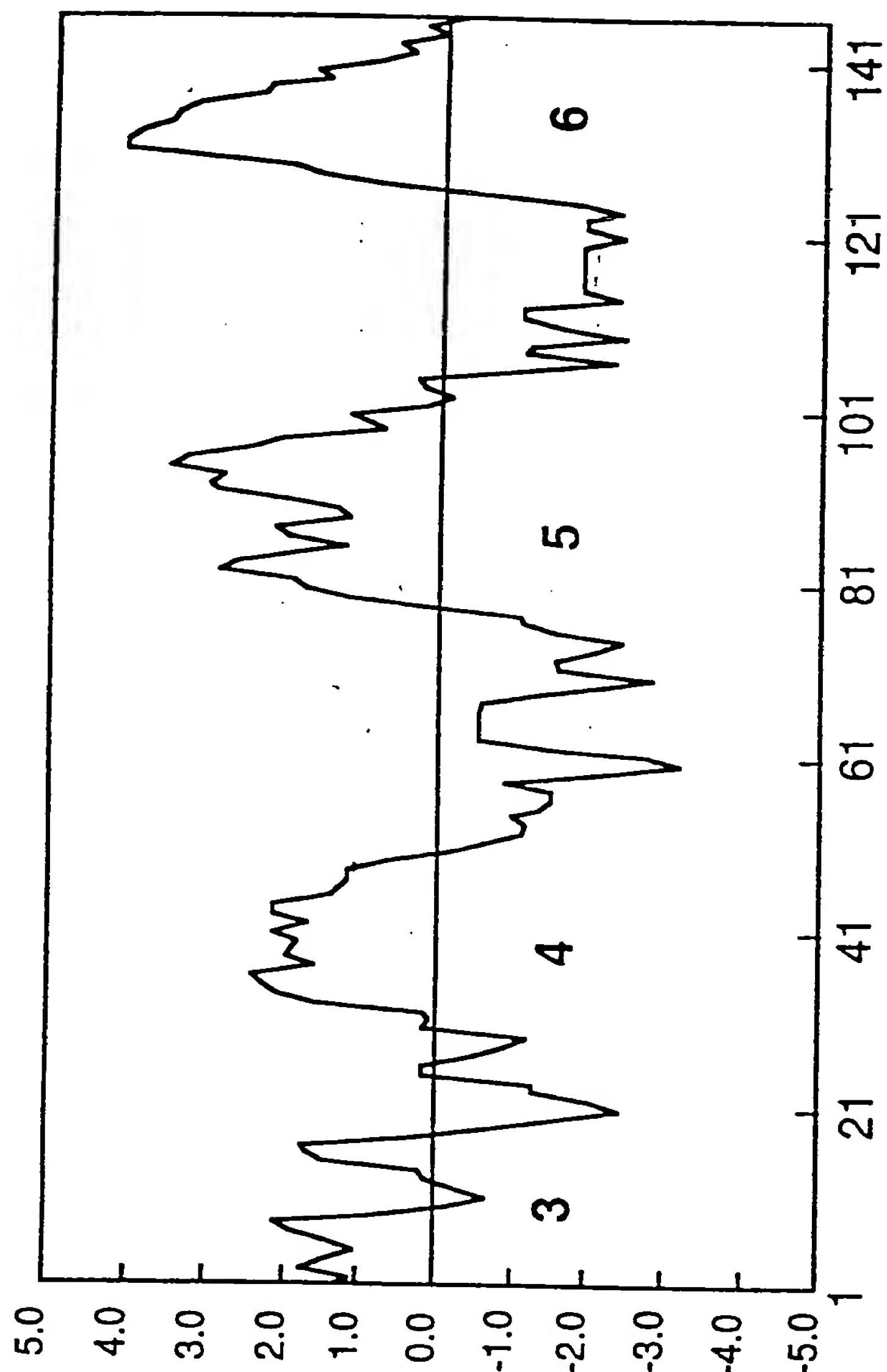
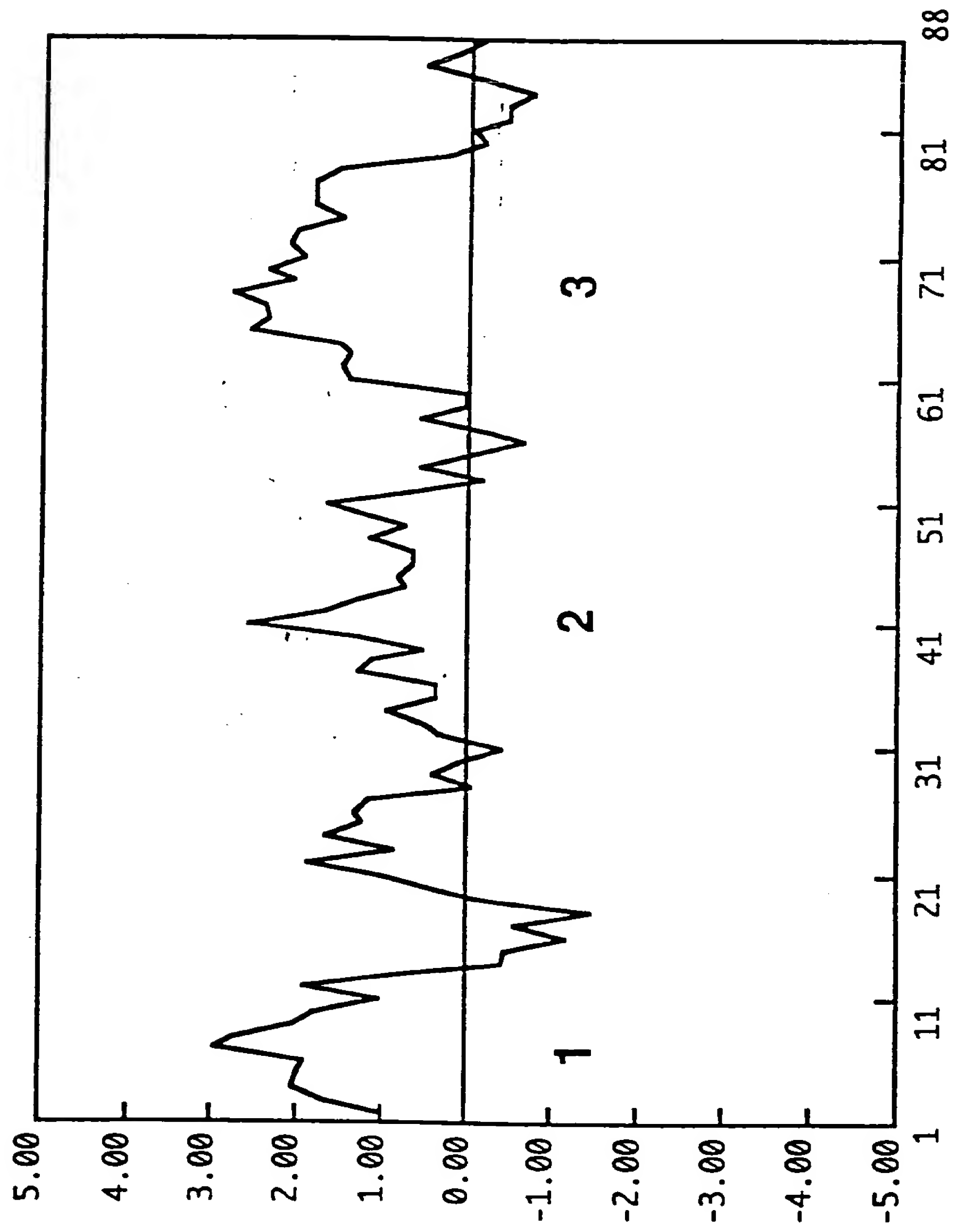


FIGURE 42

p3H2-34	1	VGLVGNFLAA	MSVDRYVAIV	HSRRSSSLRV	SRNALGVGF	IMALLSTAMAS	50
JN0605	1	MFTSVFGLIV	LSVDRYVAIV	HPLRAATYRR	PSVAKLINEG	VMLA SHLVIL	50
B41795	1	QFTSTFGLIV	MSIDRYLAIV	HPIKSAKWR	PRPAKMLTMA	VMEVSLVIT	50
A39297	1	MFTSIYCLIV	LSVDRYVAIV	HPIKAAKYRR	PIVAKVNLG	VMLLSLVIL	50
p3H2-34	51	PVA-YHORLF	HRDSNQTF	EQWPNKLHK-	-KAVVCTFV	FGYLLPLLI	100
JN0605	51	PFAFAATRP	ARGQAVACN	LQWPHPAWS-	-AVEVAYTF	LGFLLPVLA	100
B41795	51	PIVIYAGLRS	NQWGRSS-CT	INWPGESGAW	YTGFIYTF	LGFLVPLFI	100
A39297	51	PIVVFSTRTA	NSDGIVA-CN	MLMPEPAQRW	LVGEVL YTF	MGFLLPVGA	100
p3H2-34	101	CFQY----	AK	VLNHLHKKLK	NMSKKSEASK	VAVFALCMLF	150
JN0605	101	GLCYLFIHVK	MRAVALRAGW	QQRKRSE---	KKITRLVLMV	VAVFVLCWMP	150
B41795	101	CLCYLFIHVK	VKSSGIRVGS	SKRKXSE---	KKVTRMVSTV	VAVFIFCWL	150
A39297	101	CLCYVLIHAK	MRMVALKAGW	QQRKRSE---	RKITLMVMV	VAVFVICWME	150
p3H2-34	151	FY.....	200
JN0605	151	FY.....	200
B41795	151	FY.....	200
A39297	151	FY.....	200

5'	10	19	28	37	46	55
GTG GGC ATG GTG GTG GGC AAC GTC CTC GTG	Val Gly Met Val Gly Asn Val Leu	Val Leu Trp Phe Phe Gly Phe Ser Ile Lys				
---	---	---	---	---	---	---
Val Gly Met Val Gly Asn Val Leu	Val Leu Trp Phe Phe Gly Phe Ser Ile Lys					
---	---	---	---	---	---	---
AGG ACC CCC TTC TCC TCC TAC TTC	Arg Thr Pro Phe Ser Val Tyr Phe Leu His Leu Ala Ser Ala Asp Gly Ala Tyr					
---	---	---	---	---	---	---
Arg Thr Pro Phe Ser Val Tyr Phe Leu His Leu Ala Ser Ala Asp Gly Ala Tyr						
---	---	---	---	---	---	---
CTC TTC AGC AAG GGC GTG TTC TCC CTC	Leu Phe Ser Lys Ala Val Phe Ser Leu Leu Asn Ala Gly Gly Phe Leu Gly Thr					
---	---	---	---	---	---	---
Leu Phe Ser Lys Ala Val Phe Ser Leu Leu Asn Ala Gly Gly Phe Leu Gly Thr						
---	---	---	---	---	---	---
TTC GCC CAC TAT GTG CCG AGC GTG GCC CCG GTG	TTC GCC CAC TAT GTG CCG AGC GTG GCC CCG GTG					
---	---	---	---	---	---	---
Phe Ala His Tyr Val Arg Ser Val Ala Arg Val Leu Gly Leu Cys Ala Phe Val						
---	---	---	---	---	---	---
GCG GGC GTG AGC CTC CCG CCG GCG GTG AGC ATG GAG CGC TGC TGC TCT G 3'						
---	---	---	---	---	---	---
Ala Gly Val Ser Leu Leu Pro Ala Val Ser Met Glu Arg Cys Ala Ser						

FIGURE 44



1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

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FIGURE 45

pMD4	10	20	30	40	50	
A35639	1 VGMVGNV LVL	WFFGESIKRT	PFSVYFHLHA	SADGAYLFESK	AVFS LINAAGG	50
	1 CGLVGNGLVL	WFFGESIKRT	PFSIYFHLHA	SADGIYLFESK	AVIALINMGT	50
pMD4	60	70	80	90	100	
A35639	51 FLGTFAHYVR	SVA RVL GLCA	FVAGVSL LPA	VSMERCA S	100
	51 FLGSEFPDYVR	RVS RIV GLCT	FFAGVSL LPA	ISTERCVS	100

FIGURE 46

1	CAAAGCAACAGGTGCAACCTCAAGGCACTGAAAGCAAGGGGACGCAGCTCACAAGGGCCAAGGGATTGAACC	72
1		1
73	CATAACCGCTCAGAAGATTCTCCGCTGCGGAGAGCTGCGGAGGAGTCCCACCCGTCAGCTTGCTGACTGC	144
1		1
145	GAGCAGTGAGAGTCGCCTAGACCCGTACCTCTGTGTTCTGGAGCCTGCCGCCCGCACGGGAAAGGCTTAG	216
1		1
217	CTCGGGAAGTTGCAGCACCGCCTCCTCTTTAGCCAGGCCAGGCACGAGGATAGTGTGATCGGGCACAGCCAGG	288
1		1
289	GTCGCTCTTCCAGGCTTTCTTGGCGGTGCGGGAGGTACTAGTTGGAGACGCGCGCGCTCGCTCTCGCCGCT	360
1		1
361	CTGTCTTGGGCCACTCCGTGATCCTAGGCTACCTCCAGAGCCAGTTTTCCTGGCTGGCACAACCTCTCCAGG	432
1		1
433	GCGCTCCGGTCCGTTGCACAGCGCCCCAAGGGGGTATCCCAGTAAGTGATGGAAGTGGCTATGGTGAACCTC	504
1	MetGluLeuAlaMetValAsnLeu	8
505	AGTGAAGGGAATGGGAGCGACCCAGAGCCGCCAGCCCCGGAGTCCAGGCCGCTCTTCGGCATTTGGCGTGGAG	576
8	SerGluGlyAsnGlySerAspProGluProProAlaProGluSerArgProLeuPheGlyIleGlyValGlu	32
577	AACTTCATTACGCTGGTAGTGTGTTGGCCTGATTTTCGGGATGGGCGTGCTGGGCAACAGCCTGGTGATCACC	648
32	AsnPheIleThrLeuValValPheGlyLeuIlePheAlaMetGlyValLeuGlyAsnSerLeuValIleThr	56
649	GTGCTGGCGCGCAGCAAACCAGGCAAGCCGCGCAGCACCACCAACCTGTTTATCCTCAATCTGAGCATCGCA	720
56	ValLeuAlaArgSerLysProGlyLysProArgSerThrThrAsnLeuPheIleLeuAsnLeuSerIleAla	80
721	GACCTGGCCTACCTGCTCTTCTGCATCCCTTTTCAGGCCACCGTGTATGCACTGCCACCTGGGTGCTGGGC	792
80	AspLeuAlaTyrLeuLeuPheCysIleProPheGlnAlaThrValTyrAlaLeuProThrTrpValLeuGly	104
793	GCCTTCATCTGCAAGTTTATACACTACTTCTTCACCGTGTCCATGCTGGTGAGCATCTTCACCCCTGGCCGCG	864
104	AlaPheIleCysLysPheIleHisTyrPhePheThrValSerMetLeuValSerIlePheThrLeuAlaAla	128
865	ATGTCTGTGGATCGCTACGTGGCCATTTGTGCACTCGCGGCGCTCCTCCTCCCTCAGGGTGTCCCGCAACGCA	936
128	MetSerValAspArgTyrValAlaIleValHisSerArgArgSerSerSerLeuArgValSerArgAsnAla	152
937	CTGCTGGGCGTGGGCTTCATCTGGGCGCTGTCCATCGCCATGGCCTCGCCGGTGGCCTACCACCAGCGTCTT	1008
152	LeuLeuGlyValGlyPheIleTrpAlaLeuSerIleAlaMetAlaSerProValAlaTyrHisGlnArgLeu	176
1009	TTCCATCGGGACAGCAACCAGACCTTCTGCTGGGAGCAGTGGCCCAACAAGCTCCACAAGAAGGCTTACGTG	1080
176	PheHisArgAspSerAsnGlnThrPheCysTrpGluGlnTrpProAsnLysLeuHisLysLysAlaTyrVal	200
1081	GTGTGCACTTTTCGTCTTTGGGTACCTTCTGCCCTTACTGCTCATCTGCTTTTGCTATGCCAAGGTCTTAAT	1152
200	ValCysThrPheValPheGlyTyrLeuLeuProLeuLeuLeuIleCysPheCysTyrAlaLysValLeuAsn	224
1153	CATCTGCATAAAAAGCTGAAAAACATGTCAAAAAGTCTGAAGCATCCAAGAAAAGACTGCACAGACCGTC	1224
224	HisLeuHisLysLysLeuLysAsnMetSerLysLysSerGluAlaSerLysLysLysThrAlaGlnThrVal	248
1225	CTGGTGGTCTGTGTAGTATTGTCATATCCTGGCTGCCCCATCATGTCTGCCACCTCTGGGCTGAGTTTGGA	1296
248	LeuValValValValValPheGlyIleSerTrpLeuProHisHisValValHisLeuTrpAlaGluPheGly	272
1297	GCCTTCCCACTGACGCCAGCTTCCTTCTTCTTCAGAATCACCGCCCATTCCTGGCATAACGCAACTCCTCA	1368
272	AlaPheProLeuThrProAlaSerPhePhePheArgIleThrAlaHisCysLeuAlaTyrSerAsnSerSer	296
1369	GTGAACCCCATCATATATGCTTTCTCTCAGAAAACCTCCGGAAGGCGTACAAGCAAGTGTTCAGTGTTCAT	1440
296	ValAsnProIleIleTyrAlaPheLeuSerGluAsnPheArgLysAlaTyrLysGlnValPheLysCysHis	320
1441	GTTTGGGATGAATCTCCACGCAGTGAAACTAAGGAAAACAAGAGCCGGATGGACACCCCGCCATCCACCAAC	1512
320	ValCysAspGluSerProArgSerGluThrLysGluAsnLysSerArgMetAspThrProProSerThrAsn	344
1513	TGCACCCACGTGTGAAGGTTTGGCGGAGCCTCCCGACTTCCAGCTCCCATGTGTGTAGAGAGAGGAGGGCG	1584
344	CysThrHisVal***	349
1585	GAGCGAATTATCAAGTAACATGG	1607
349		349

FIGURE 47

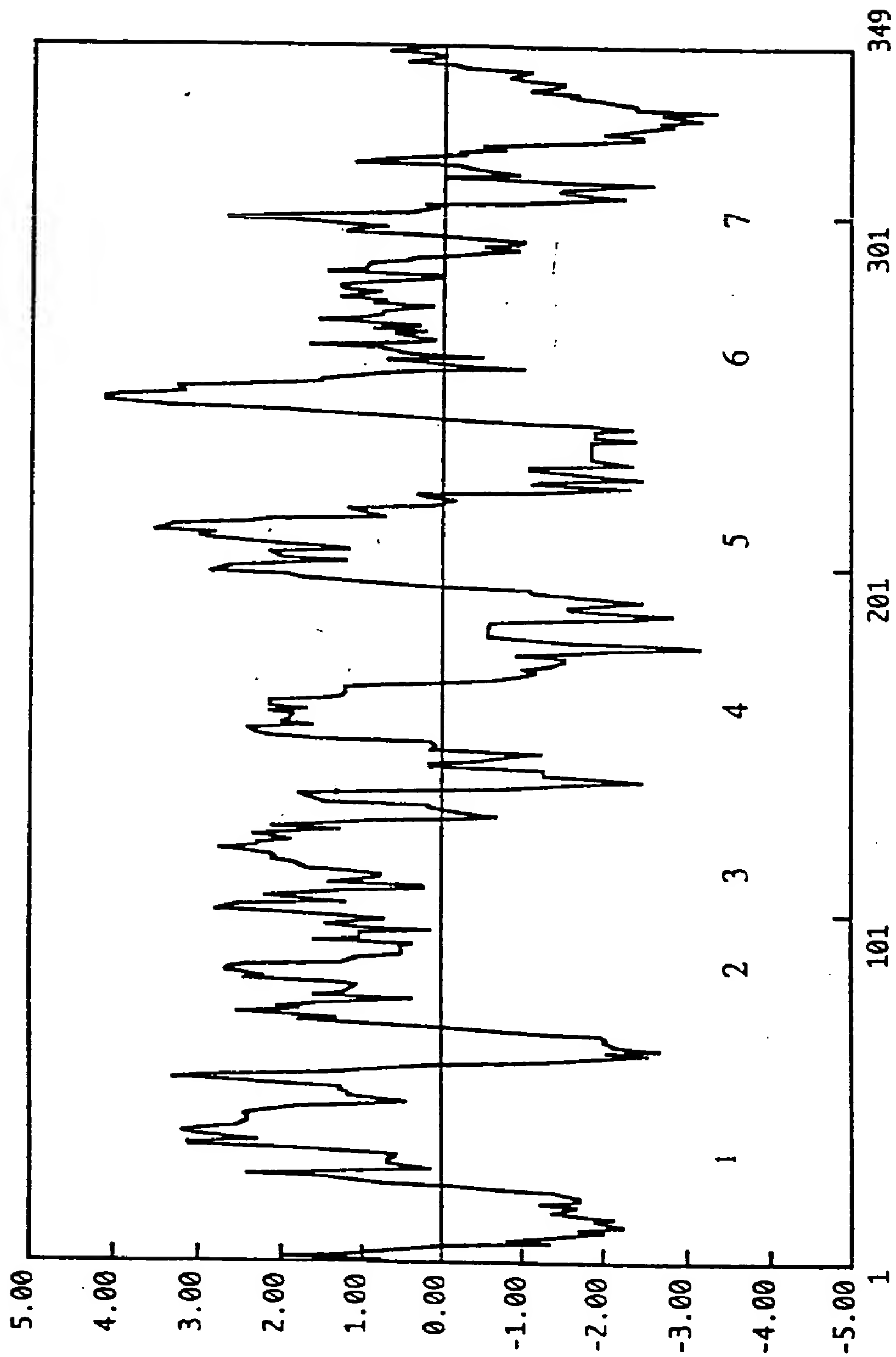


FIGURE 48

MOUSEGALRECE HUMGALAMI	1	10	20	30	40	50
	1	MELAVNLSE MELAVNLSE	GNSSDPEPPA GNSSDPEPPA	PEPSRPLEFGIG PEPSRPLEFGIG	VENFITLAVF VENFITLAVF	QHTFAMGVHG QHTFAMGVHG
MOUSEGALRECE HUMGALAMI	51	60	70	80	90	100
	51	NSLVITVLR NSLVITVLR	SKPGKPRSTT SKPGKPRSTT	NLFILNLSIA NLFILNLSIA	DHAYITFOIP DHAAYITFOIP	EQATVVALPT EQATVVALPT
MOUSEGALRECE HUMGALAMI	101	110	120	130	140	150
	101	WVLGAFICKF WVLGAFICKF	IHYFFTVSMT IHYFFTVSMT	VSIFTLAAMS VSIFTLAAMS	VPRYVAIVHS VDRYVAIVHS	RRSSSLRVSR RRSSSLRVSR
MOUSEGALRECE HUMGALAMI	151	160	170	180	190	200
	151	NALLGVGCIW NALLGVGCIW	ALSTAMASPV ALSTAMASPV	AYHQRLEH-R AYHQRLEH-R	DSNOTFCWEO ASNOTFCWEO	WPNKLEHKKAY WPNKLEHKKAY
MOUSEGALRECE HUMGALAMI	201	210	220	230	240	250
	201	WCTFVEGYL WCTFVEGYL	LPLLLICFCY LPLLLICFCY	AKVLANHLHKK AKVLANHLHKK	LKNMSKKSEA LKNMSKKSEA	SKKKTATQTVL SKKKTATQTVL
MOUSEGALRECE HUMGALAMI	251	260	270	280	290	300
	251	VVVVFGISW VVVVFGISW	LPHHIIHLWA LPHHIIHLWA	EFGVFPITPA EFGVFPITPA	SEFERITAHG SEFERITAHG	LAYSNSNVNP LAYSNSNVNP
MOUSEGALRECE HUMGALAMI	301	310	320	330	340	350
	301	IYYAFLSENF IYYAFLSENF	RKAYKQVFKC RKAYKQVFKC	HVCDESPRSE HVCDESPRSE	TKENKSRMDT TKENKSRMDT	PPSTNCTHVX PPSTNCTHVX
MOUSEGALRECE HUMGALAMI	351	360	370	380	390	400
	351
MOUSEGALRECE HUMGALAMI	351	X.....

FIGURE 49

5'	CTC	GCG	GCT	CTG	GGT	ATG	GAT	CGG	TAT	CTT	CTC	ACC	CTT	CAC	CCA	GTG	TGG	TCC	
										Leu	Leu	Thr	Leu	His	Pro	Val	Trp	Ser	
	CAA	AAG	CAC	CGA	ACC	TCA	CAC	TGG	GCT	TCC	AGA	GTC	GTT	CTG	GGA	GTC	TGG	CTC	
	Gln	Lys	His	Arg	Thr	Ser	His	Trp	Ala	Ser	Arg	Val	Val	Leu	Gly	Val	Trp	Leu	
	TCT	GCC	ACT	GCC	TTC	AGC	GTG	CCC	TAT	TTG	GTT	TTC	AGG	GAG	ACA	TAT	GAT	GAC	
	Ser	Ala	Thr	Ala	Phe	Ser	Val	Pro	Tyr	Leu	Val	Phe	Arg	Glu	Thr	Tyr	Asp	Asp	
	CGT	AAA	GGA	AGA	GTG	ACC	TGC	AGA	AAT	AAC	TAC	GCT	GTG	TCC	ACT	GAC	TGG	GAA	
	Arg	Lys	Gly	Arg	Val	Thr	Cys	Arg	Asn	Asn	Tyr	Ala	Val	Ser	Thr	Asp	Trp	Glu	
	AGC	AAA	GAG	ATG	CAA	ACA	GTA	AGA	CAA	TGG	ATT	CAT	GCC	ACC	TGT	TTC	ATC	AGC	
	Ser	Lys	Glu	Met	Gln	Thr	Val	Arg	Gln	Trp	Ile	His	Ala	Thr	Cys	Phe	Ile	Ser	
	CGC	TTC	ATA	CTG	GGC	TTC	CTT	CTG	CCT	TTC	TTA	GTC	ATT	GGC	TTT	TGT	TAT	GAA	
	Arg	Phe	Ile	Leu	Gly	Phe	Leu	Leu	Pro	Phe	Leu	Val	Ile	Gly	Phe	Cys	Tyr	Glu	
	AGA	GTA	GCC	CGC	AAG	ATG	AAA	GAG	AGG	GGC	CTC	TTT	AAA	TCC	AGC	AAA	CCC	TTC	
	Arg	Val	Ala	Arg	Lys	Met	Lys	Glu	Arg	Gly	Leu	Phe	Lys	Ser	Ser	Lys	Pro	Phe	
	AAA	GTC	ACG	ATG	ACT	GCT	GTT	ATC	TCT	TTT	TTC	TGT	CCT	GGC	TTC	CCT	ACC	ACA	
	Lys	Val	Thr	Met	Thr	Ala	Val	Ile											

TG 3'

FIGURE 50

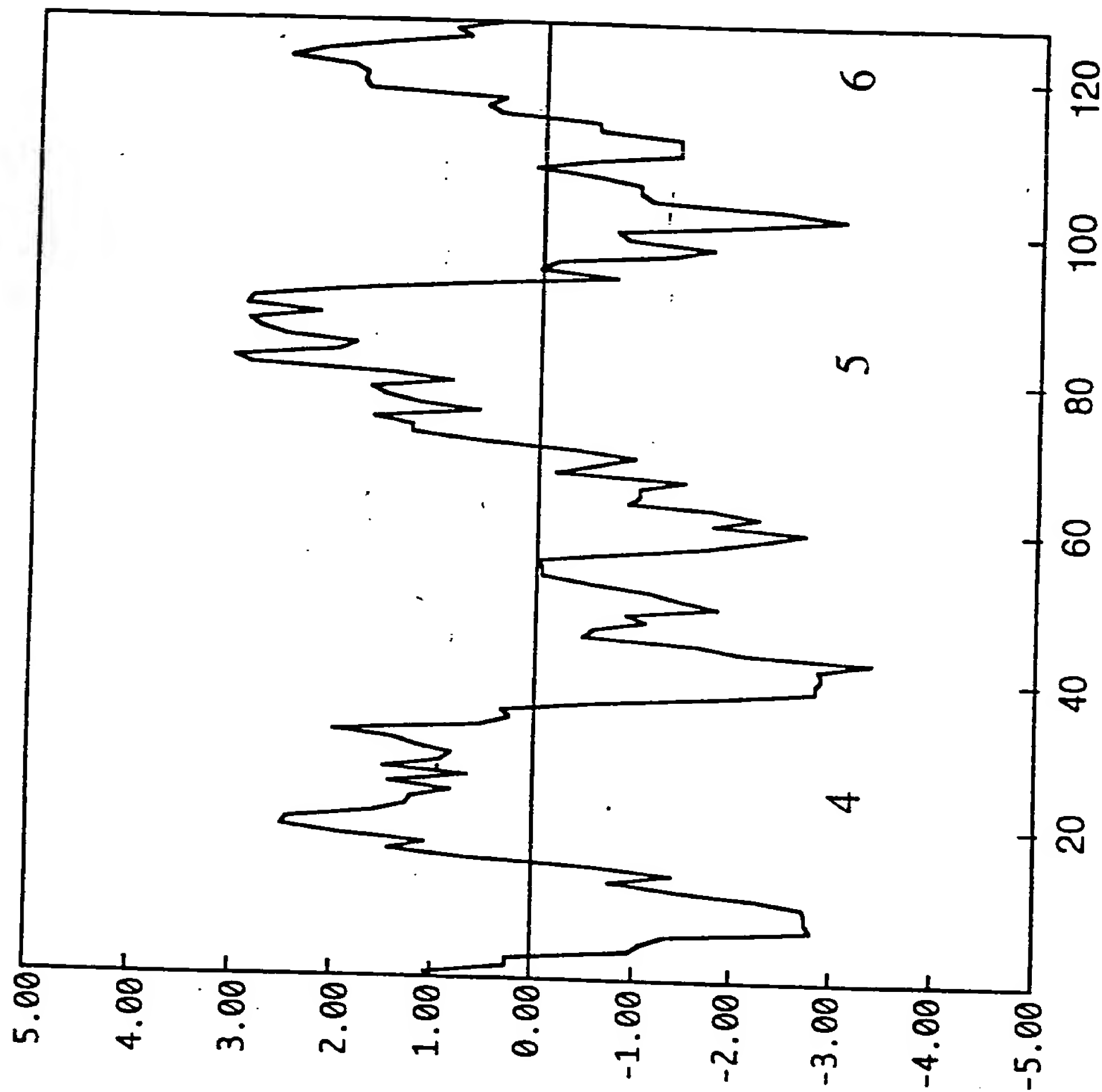


FIGURE 51

pmj10	1	10	20	30	40	50	50
B42009	1	1	1	1	1	1	50
JC2014	1	1	1	1	1	1	50
A46520	1	1	1	1	1	1	50
A46525	1	1	1	1	1	1	50
S28787	1	1	1	1	1	1	50
pmj10	51	60	70	80	90	100	100
B42009	51	51	51	51	51	51	100
JC2014	51	51	51	51	51	51	100
A46520	51	51	51	51	51	51	100
A46525	51	51	51	51	51	51	100
S28787	51	51	51	51	51	51	100
pmj10	101	110	120	130	140	150	150
B42009	101	101	101	101	101	101	150
JC2014	101	101	101	101	101	101	150
A46520	101	101	101	101	101	101	150
A46525	101	101	101	101	101	101	150
S28787	101	101	101	101	101	101	150

[illegible]

FIGURE 53

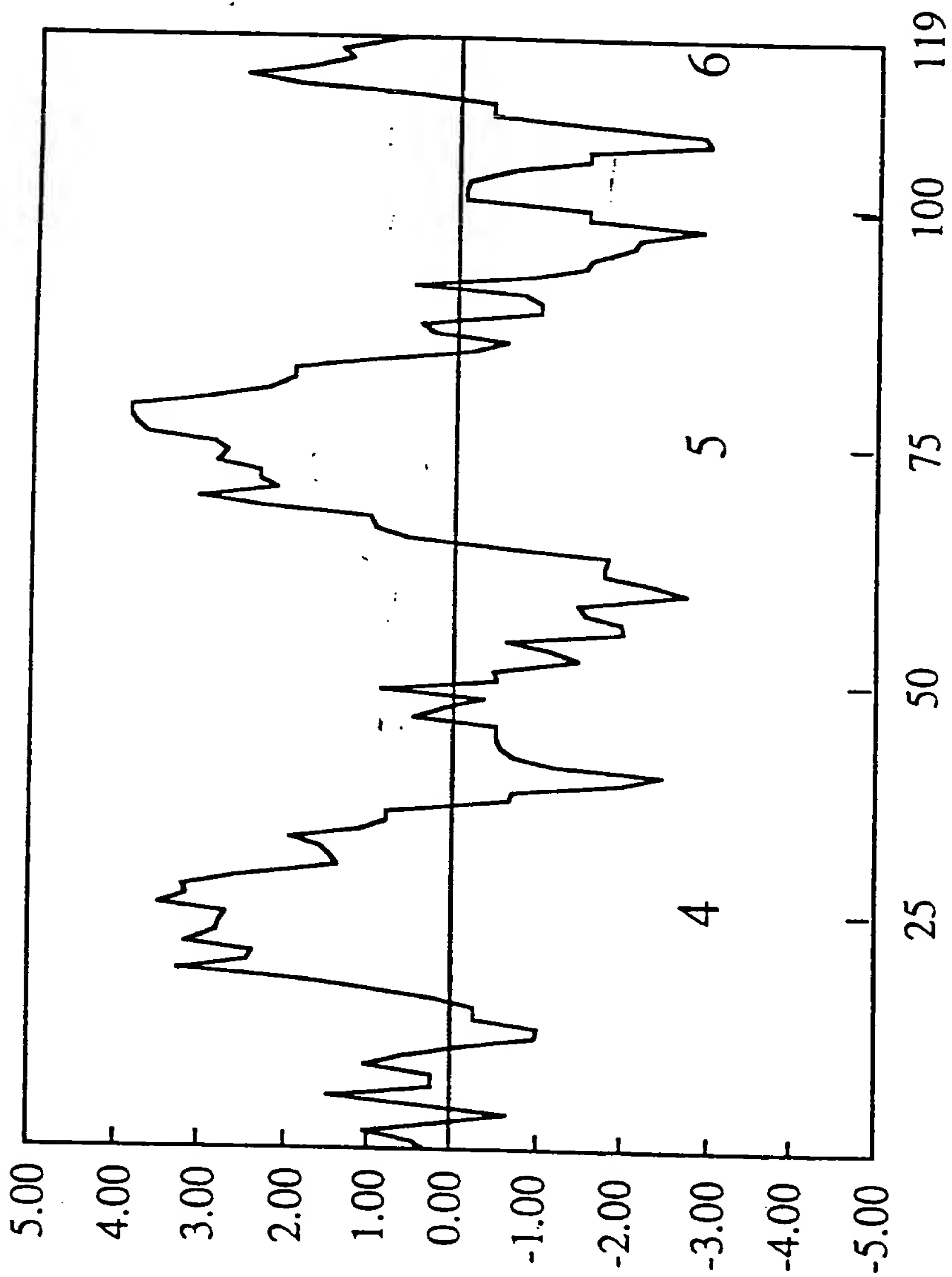


FIGURE 54

pMH28	10	20	30	40	50
P35343	1 FKIVKPLST	FIOSVNYSKL	VSLVWLLML	LIAVPNVILT	NQRVKDVTOI
A41795	1 LAIVHATSP-	LQKRHLVKF	VCIAMWLESV	IEALPILITR	NPVKVNLSTL
A47457	1 VAVVHPKAA	RYRRPTVAKV	VNLGVWVESL	LVI LPFVFS	RTPAANSDCIV
	1 VAVVHPLRAA	TYRRPSVAKL	INLGVNLASE	LVT ERIAIFA	DTRPARGGO-
pMH28	60	70	80	90	100
P35343	51 KCMELKNEL	GRQWHKASNY	IFVGI F-WLV	FLLILIFYTA	IT-RKIFKSH
A41795	51 VCYEEDVGNT	SRL--RVLRL	ILPQTEGELV	PLLIMLFCYG	FTLRPLFKAH
A47457	51 AQNM-LMPEP	AQRWLVGFEV-	LYTFLLMGEFL	PVGATCLCYV	LHILAKMRMVA
	51 AVAC-NLQWP	HPA WSAVEV-	VYTFLLGEFL	PVLAIGLCYL	LIVGKMRAVA
pMH28	110	120	130	140	150
P35343	101 LKSRKNSI-S	VKKKSSRNIF	S--IV....
A41795	101 MG----QKRR	AMR----VIF	AVLV....
A47457	101 LKAGWQQRKR	SEKITTLMVM	MVMV....
	101 LKAGWQQRKR	SEKITTLLVL	MVMV....

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FIGURE 55

5' GCC ACC AAC GTG TTC ATC CTG TGT CTG GTG GAC CTG CTG GCT GCC CTG ACC CTC

 Val Asp Leu Leu Ala Ala Leu Thr Leu

ATG CCT CTG GCC ATG CTC TCC AGC TCC GCC CTC TTT GAC CAC GCC CTC TTT GGG

 Met Pro Leu Ala Met Leu Ser Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly

GAG GTG GCC TGC CGC CTC TAC TTG TTC CTG AGC GTC TGC TTT GTC AGC CTG GCC

 Glu Val Ala Cys Arg Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu Ala

ATC CTC TCG GTG TCC GCC ATC AAT GTG GAG CGC TAC TAT TAT GTG GTC CAC CCC

 Ile Leu Ser Val Ser Ala Ile Asn Val Glu Arg Tyr Tyr Tyr Val Val His Pro

ATG CGC TAT GAG GTG CGC ATG AAA CTG GGG CTG GTG GCC TCT GTG CTG GTG GGC

 Met Arg Tyr Glu Val Arg Met Lys Leu Gly Leu Val Ala Ser Val Leu Val Gly

GTG TGG GTG AAG GCC CTG GCC ATG GCT TCT GTG CCA GTG TTG GGA AGG GTG TCC

 Val Trp Val Lys Ala Leu Ala Met Ala Ser Val Pro Val Leu Gly Arg Val Ser

TGG GAG GAA GGC CCT CCC AGT GTC CCC CCA GGC TGT TCA CTC CAA TGG AGC CAC

 Trp Glu Glu Gly Pro Pro Ser Val Pro Pro Gly Cys Ser Leu Gln Trp Ser His

AGT GCC TAC TGC CAG CTT TTC GTG GTG GTC TTC GCC GTC CTC TAC TTC CTG CTG

 Ser Ala Tyr Cys Gln Leu Phe Val Val Val Phe Ala Val Leu Tyr Phe Leu Leu

CCC CTG CTC CTC ATC CTT GTG GTC TAC TGC AGC ATG TTC CGG GTG GCT CGT GTG

 Pro Leu Leu Leu Ile Leu Val Val Tyr Cys Ser Met Phe Arg Val Ala Arg Val

GCT GCC ATG CAG CAC GGG CCG CTG CCC ACG TGG ATG GAG ACG CCC CGG CAA CGC

 Ala Ala Met Gln His Gly Pro Leu Pro Thr Trp Met Glu Thr Pro Arg Gln Arg

FIGURE 56

549	558	567	576	585	594
TCC GAG TCT CTC AGC AGC CGC TCC ACT ATG GTC ACC AGC TCG GGG GCC CCG CAG					
---	---	---	---	---	---
Ser Glu Ser Leu Ser Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala Pro Gln					
603	612	621	630	639	648
ACC ACC CCT CAC CGG ACG TTT GGC GGA GGG AAG GCA GCA GTG GTC CTC CTG GCT					
---	---	---	---	---	---
Thr Thr Pro His Arg Thr Phe Gly Gly Gly Lys Ala Ala Val Val Leu Leu Ala					
657	666	675	684	693	702
GTG GGA GGA CAG TTC CTG CTC TGT TGG TTG CCC TAC TTC TCC TTC CAC CTC TAT					
---	---	---	---	---	---
Val Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe Ser Phe His Leu Tyr					
711	720	729	738	747	756
GTG GCC CTG AGC GCT CAG CCC ATT GCA GCG GGG CAG GTG GAG AAC GTG GTG ACC					
---	---	---	---	---	---
Val Ala Leu Ser Ala Gln Pro Ile Ala Ala Gly Gln Val Glu Asn Val Val Thr					
765	774	783	792	801	810
TGG ATT GGC TAC TTC TGC TTC ACC TCC AAC CCT CTC CTC TAT TCC TTC CTC CCT 3'					
---	---	---	---	---	---
Trp Ile Gly Tyr Phe Cys Phe Thr Ser					

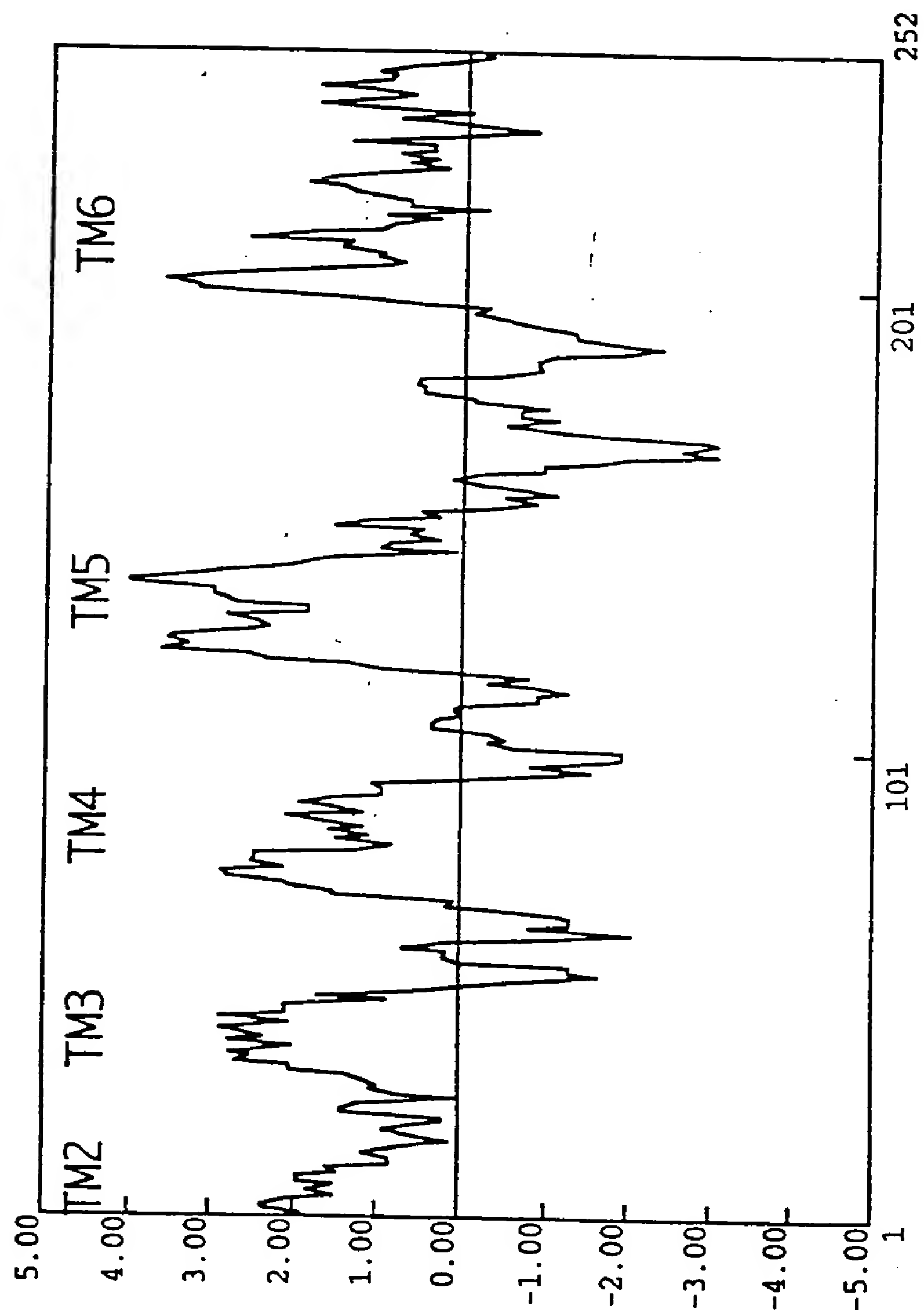


FIGURE 58

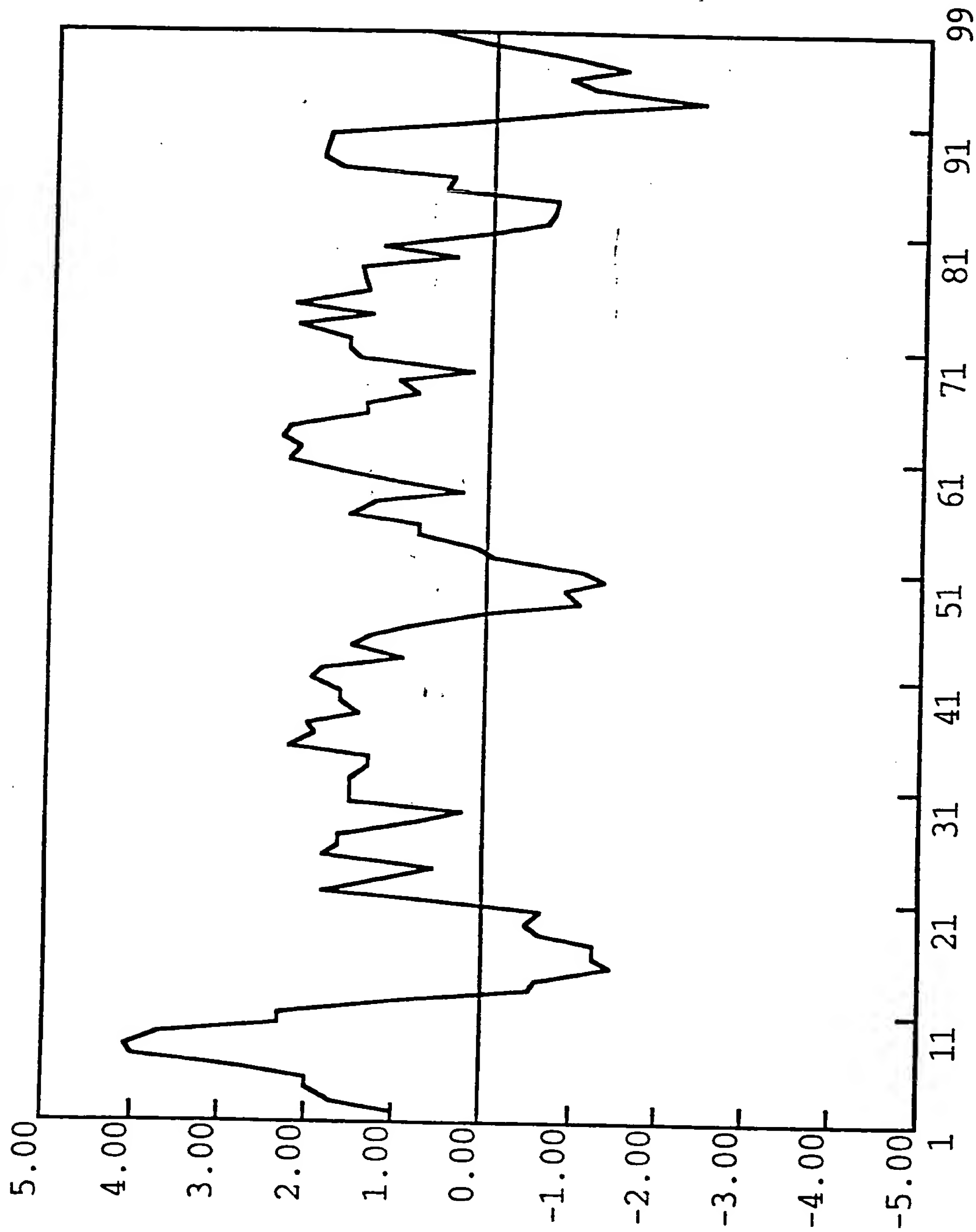


FIGURE 59

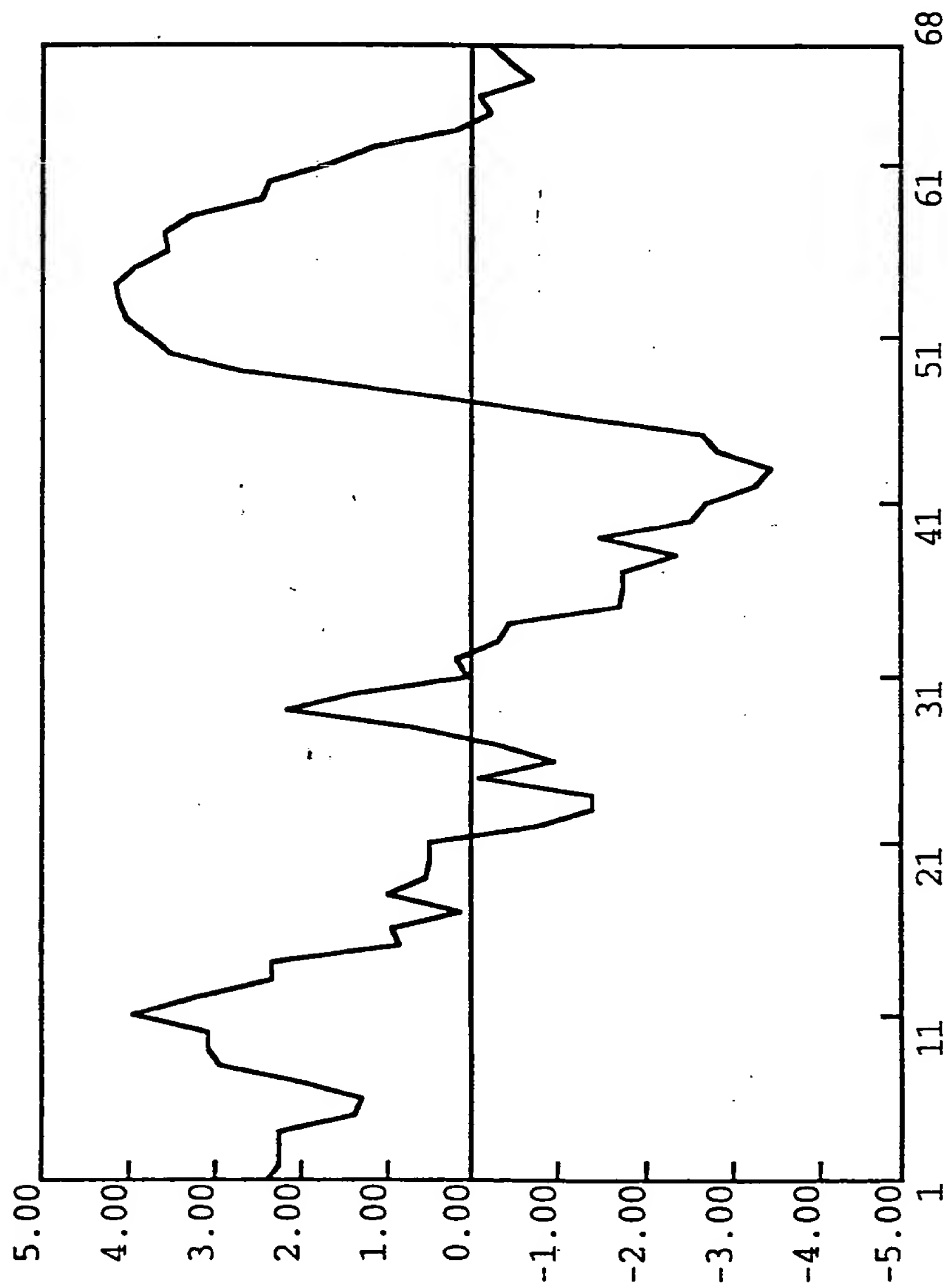


FIGURE 60

p19P2	10	20	30	40	50
S12863	1 VGMVGNVLV	LVIARVRRLLH	NVTNFIIGNI	ALSDVEMCTA	GVPLTLAYAF
	1 LGVSGNLAII	IIILKQKEMR	NVTNILLVNL	SFSDLAVAVM	CLPFTFVYIL
					50
					50
p19P2	60	70	80	90	100
S12863	51 EPRGWNVEGCG	LCHLVFELQP	VIVYVSVFTL	TTIAVDRYVV	LVHPLRRRI-
	51 MDH-WVEGET	MCKLNPVQC	VSITVSISSL	VLIAVERHQL	IINPRGWRPN
					100
					100
p19P2	110	120	130	140	150
S12863	101 -----	-----	-----	-----	-----
	101 NRHAYIGITV	IWVLAVASSL	PFVIYQILTD	EPFQNVSLAA	FKDKYVCFDK
					150
					150
p19P2	160	170	180	190	200
S12863	151 -----GLLV	TYLLPLLVIL	LS-----Y	VRVSVKLRNR	VVPGCVTQSQ
	151 FPSDSHRLSY	TTLLLVLYQYF	GPLCFIFICY	FKIYIRLKR	NNMMDKIRDS
					200
					200
p19P2	210	220	230	240	250
S12863	201 ADWDRARRRR	TFCLLVVVVV	VFAICWLPVY	-----	-----
	201 KYRSSETKRI	NVMLLSIIVA	-FAVCWLEPLT	-----	-----
					250
					250

FIGURE 61

p19P2	1	10	20	30	40	50	
PG3-2/PG1-10	1	VGMVGNVLLV	LVIAVRRLH	NVTNELIGNL	ALSDVLMCTA	CVPLTLAYAF	50
	1	VGMVGNVLLV	LVIAVRRLH	NVTNELIGNL	ALSDVLMCTA	CVPLTLAYAF	50
p19P2	51	60	70	80	90	100	
PG3-2/PG1-10	51	EPRGMVFCGG	LCHLVFFLOP	VTVVSVFTL	TTIAVDRVVV	LVHPLRRRI-	100
	51	EPRGMVFCGG	LCHLVFFLOP	VTVVSVFTL	TTIAVDRVVV	LVHPLRRRI-	100
p19P2	101	110	120	130	140	150	
PG3-2/PG1-10	101	LRLSAYAVLA	IWVLSAVLAL	PAAVHTYHVE	LKPHDVRICE	EFWGSQERQR	150
	101	LRLSAYAVLA	IWVLSAVLAL	PAAVHTYHVE	LKPHDVRICE	EFWGSQERQR	150
p19P2	151	160	170	180	190	200	
PG3-2/PG1-10	151	GLLLV	TVLLPLLVIL	LSYVRVSVKL	RNRVVPGCVT	QSOADWDRAR	200
	151	QLYAWGLLV	TVLLPLLVIL	LSYVRVSVKL	RNRVVPGCVT	QSOADWDRAR	200
p19P2	201	210	220	230	240	250	
PG3-2/PG1-10	201	RRRTECLLVV	VWVFALCWL	PYY.....	250
	201	RRRTECLLVV	VWVFALCWL	PFF.....	250

FIGURE 62

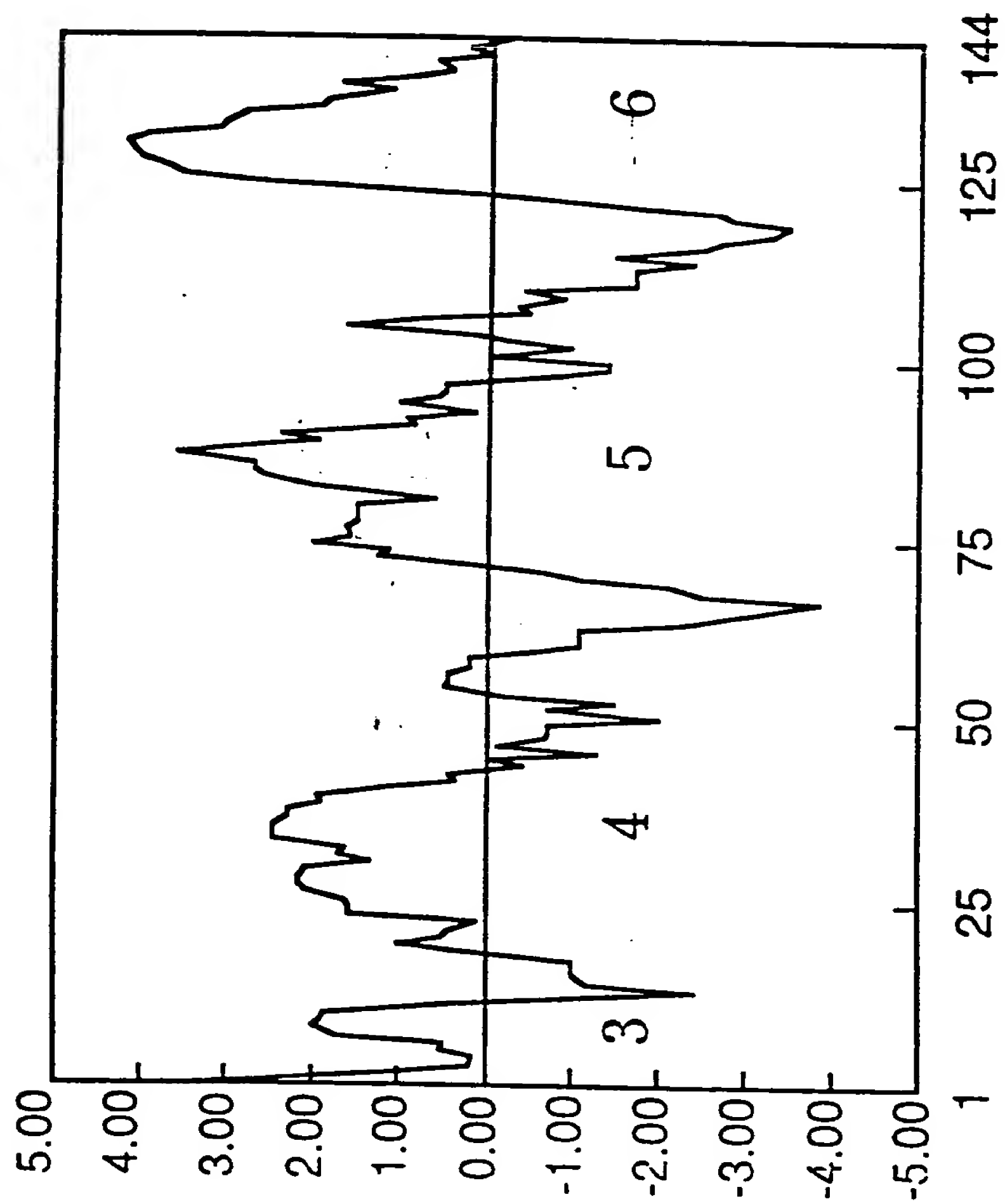
5'	CTG	TGT	9	ATC	GCG	18	GTG	GAT	AGG	27	TAC	GTG	GTT	36	CTG	GTG	CAC	45	CCG	CTA	CGT	54	CGG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Cys	Val	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg					
	CGC	ATT	63	CTG	AGG	72	CTC	AGC	GCC	81	TAC	GCG	GTG	CTG	GGC	ATC	TGG	GCT	CTA	108	TCT		
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Arg	Ile	Ser	Leu	Arg	Leu	Ser	Ala	Tyr	Ala	Val	Leu	Gly	Ile	Trp	Ala	Leu	Ser					
	GCA	GTG	117	CTG	GCG	126	CTG	CCG	GCC	GCG	135	GTG	CAC	ACC	TAC	CAT	GTG	153	GAG	CTC	AAG	162	CCC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ala	Val	Leu	Ala	Leu	Pro	Ala	Ala	Val	His	Thr	Tyr	His	Val	Glu	Leu	Lys	Pro					
	CAC	GAC	171	GTG	AGC	180	CTC	TGC	GAG	GAG	189	TTC	TGG	GGC	TCG	CAG	GAG	207	CGC	CAA	CGC	216	CAG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	His	Asp	Val	Ser	Leu	Cys	Glu	Glu	Phe	Trp	Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln					
	ATC	TAC	225	GCC	TGG	234	GGG	CTG	CTT	CTG	243	GCG	ACC	TAT	TTG	CTC	CCC	261	CTG	CTG	GCC	270	ATC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ile	Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Gly	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Ala	Ile					
	CTC	CTG	279	TCT	TAC	288	GTA	CGG	GTG	TCA	297	GTG	AAG	CTG	AGG	AAC	CGC	315	GTG	GTG	CCT	324	GGC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val	Val	Pro	Gly					
	AGC	GTG	333	ACC	CAG	342	AGT	CAA	GCT	GAC	351	TGG	GAC	CGA	GCG	CGT	CGC	369	CGC	CGC	ACT	378	TTC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg	Arg	Thr	Phe					
	TGT	CTG	387	CTG	GTG	396	GTG	GTA	GTG	TTC	405	GTG	ACG	CTC	TGC	TGG	CTG	423	CCC	TTC	432	TAC	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Phe	Thr	Leu	Cys	Trp	Leu	Pro	Phe	Tyr					

CT 3'

FIGURE 63

p19P2	1	10	20	30	40	50	
PG3-2/PG1-10	1	VGMVGNVLLV	LVIAVRREH	NVTNELIGNL	ALSDVLMCTA	CVPLTLAYAF	50
p5S38	-79	VGMVGNILEV	LVIAVRRLY	NVTNELIGNL	ALSDVLMCTA	CVPLTLAYAF	50
		-30
p19P2	51	60	70	80	90	100	
PG3-2/PG1-10	51	EPRGWNVFGG	LCHLVFELQP	VTAVVSVELL	TTIAVDRVAV	LVHPLRRRI	100
p5S38	-29	EPRGWNVFGG	LCHLVFELQA	VTAVVSVELL	TTIAVDRVAV	LVHPLRRRI	100
		CVIAVDRVAV	LVHPLRRRI	21
p19P2	101	110	120	130	140	150	
PG3-2/PG1-10	101	LRLSAYAVLA	IWL SAVLAL	PAAVHTYHVE	LKPHDVR LCE	EFWGSQERQR	150
p5S38	22	LRLSAYAVLG	IWL SAVLAL	PAAVHTYHVE	LKPHDVS LCE	EFWGSQERQR	150
		71
p19P2	151	160	170	180	190	200	
PG3-2/PG1-10	151	GLLLV	TYLLPLLVIL	LSYVRVSVKL	RNRVVPVCVT	QSOADMDRAR	200
p5S38	72	QLYAWGLLLV	TYLLPLLVIL	LSYVRVSVKL	RNRVVPGRVT	QSOADMDRAR	200
		QIYAWGLLLG	TYLLPLLVIL	LSYVRVSVKL	RNRVVPGRVT	QSOADMDRAR	121
p19P2	201	210	220	230	240	250	
PG3-2/PG1-10	201	RRRTFCLLVV	VVVFAICWL	PYY.....	250
p5S38	122	RRRTFCLLVV	VVVFTLCWL	PFF.....	250
		RRRTFCLLVV	VVVFTLCWL	PFY.....	171

FIGURE 64



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FIGURE 65

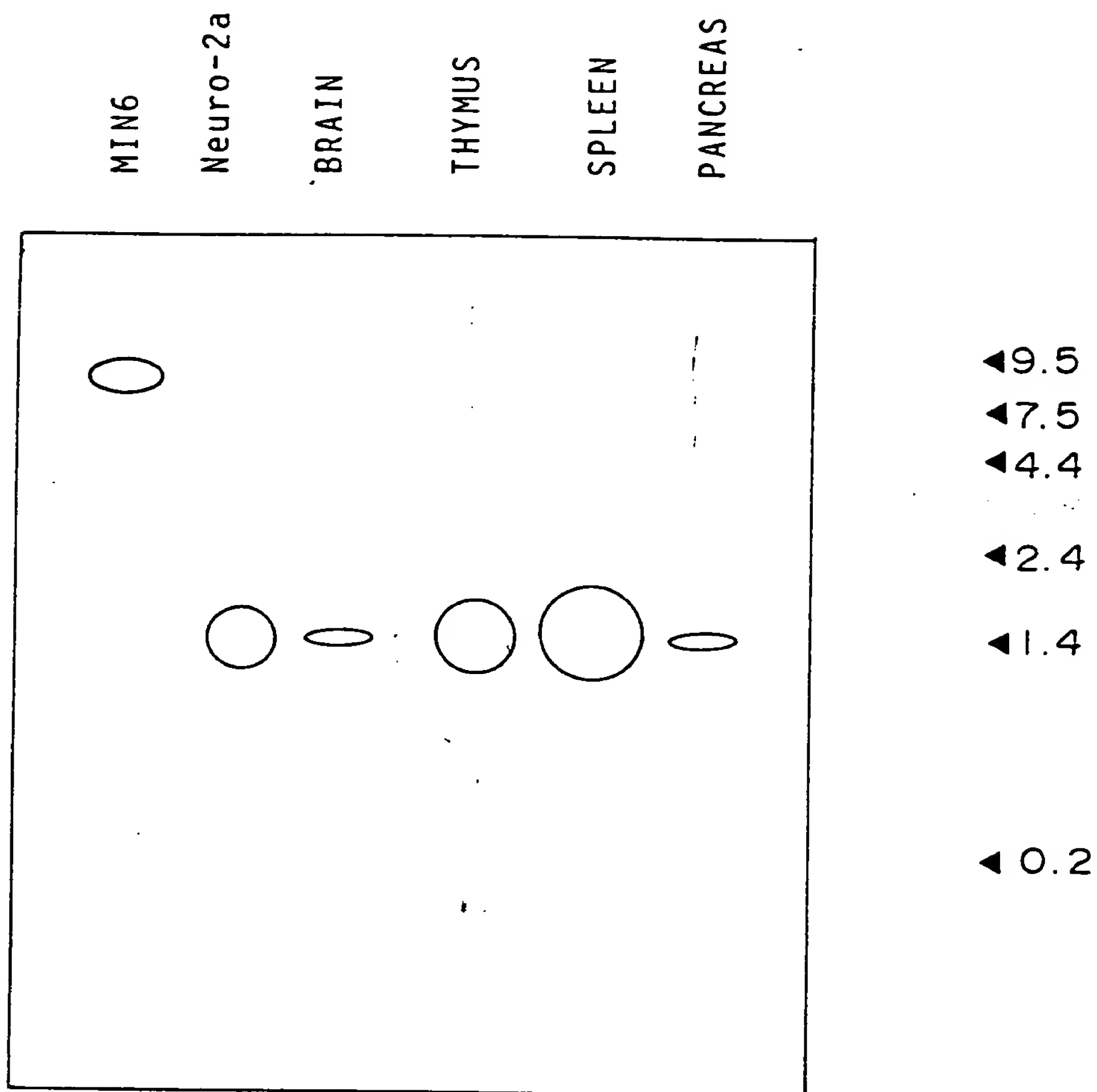
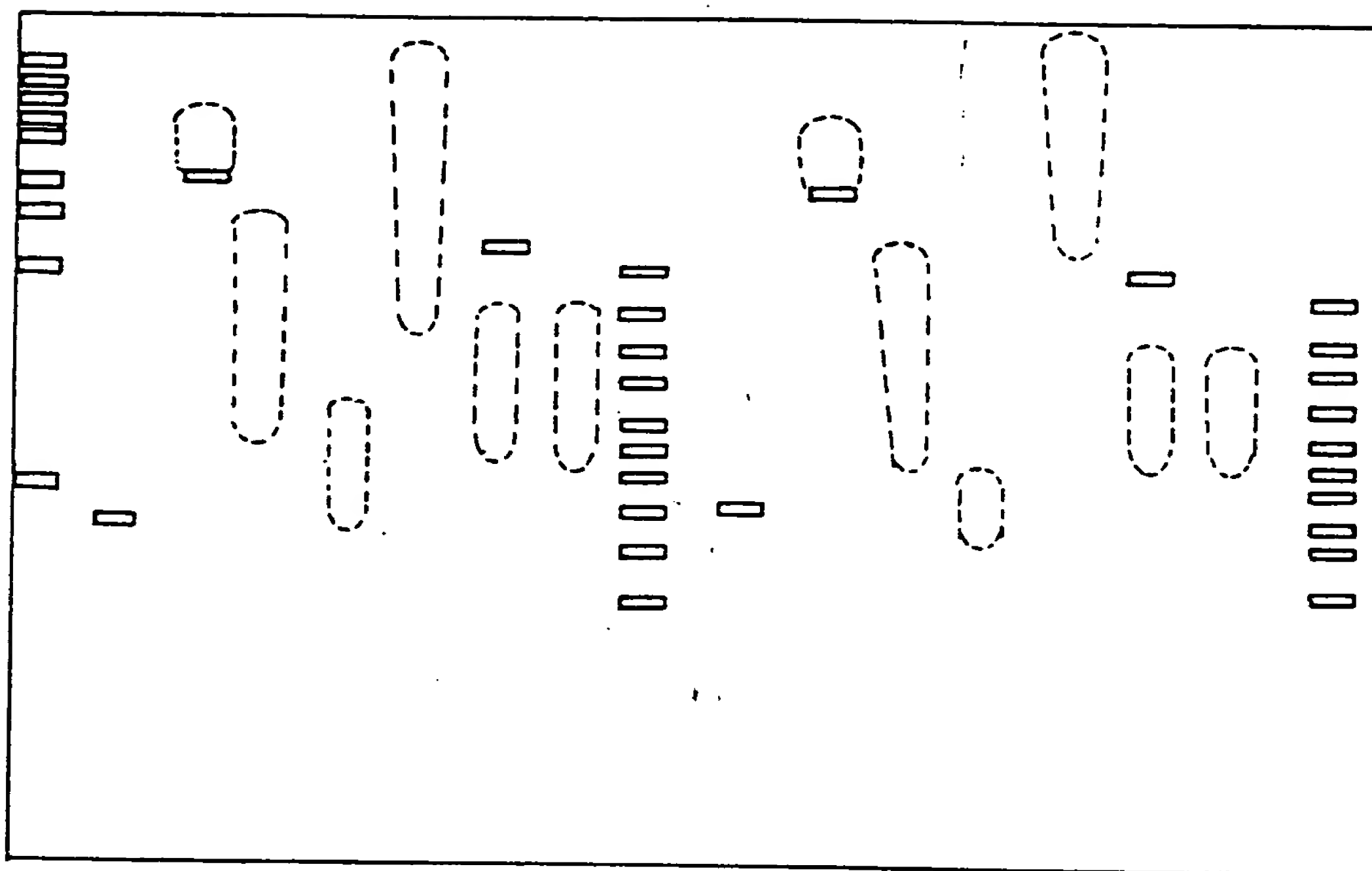


FIGURE 66

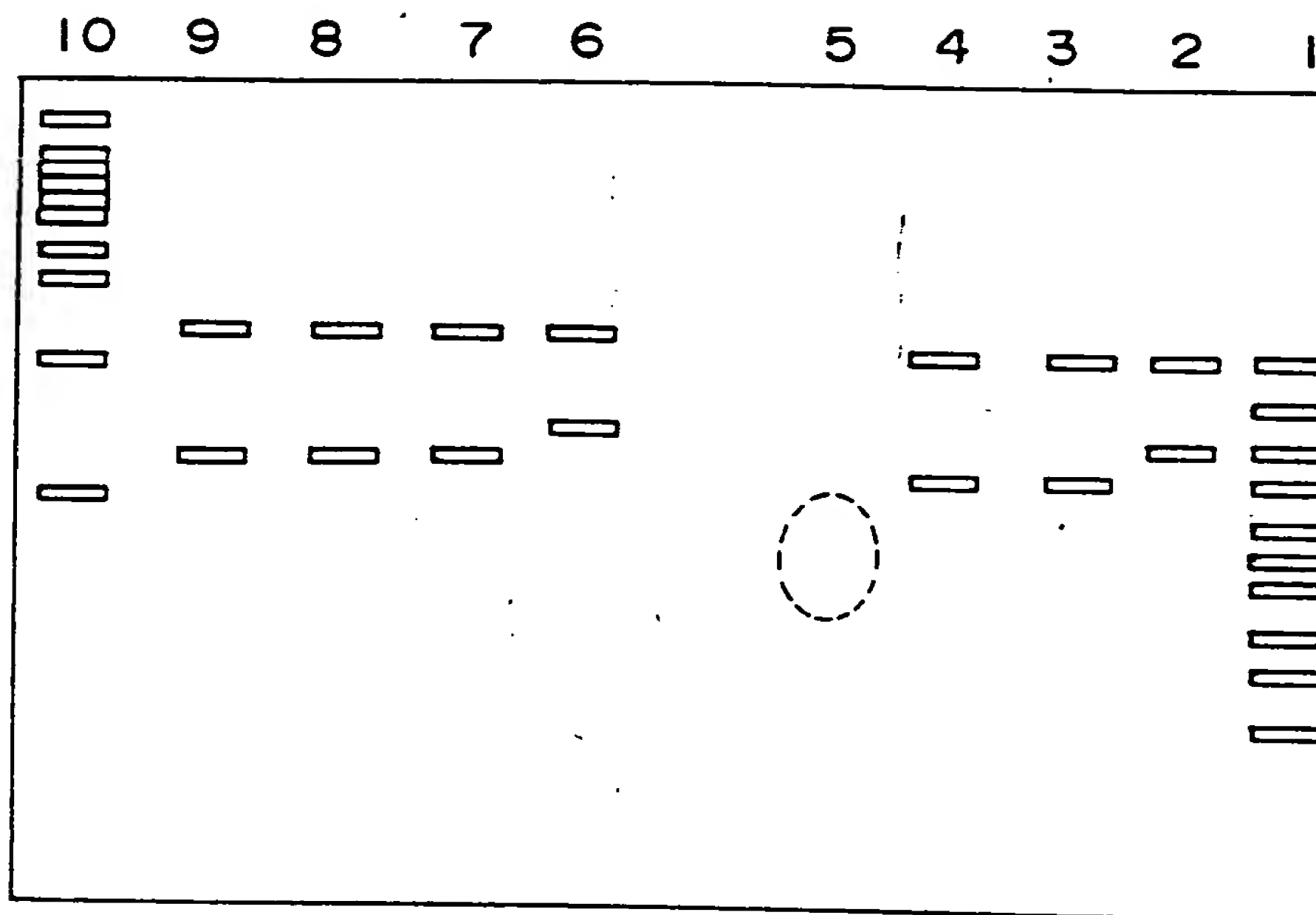
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17



מספרים אלה הם תוצאות של חישובים שנעשו על ידי מחשב וייתכן והם אינם מדויקים. המידע המוצג כאן אינו מהווה ייעוץ או המלצה. המשתמש במידע זה עלול להיחשף לסיכונים. אין להשתמש במידע זה לצורכי מסחר או להחלטות פיננסיות. המידע המוצג כאן אינו מהווה חלק ממוצר או שירות של חברתנו. המידע המוצג כאן אינו מהווה חלק ממוצר או שירות של חברתנו.

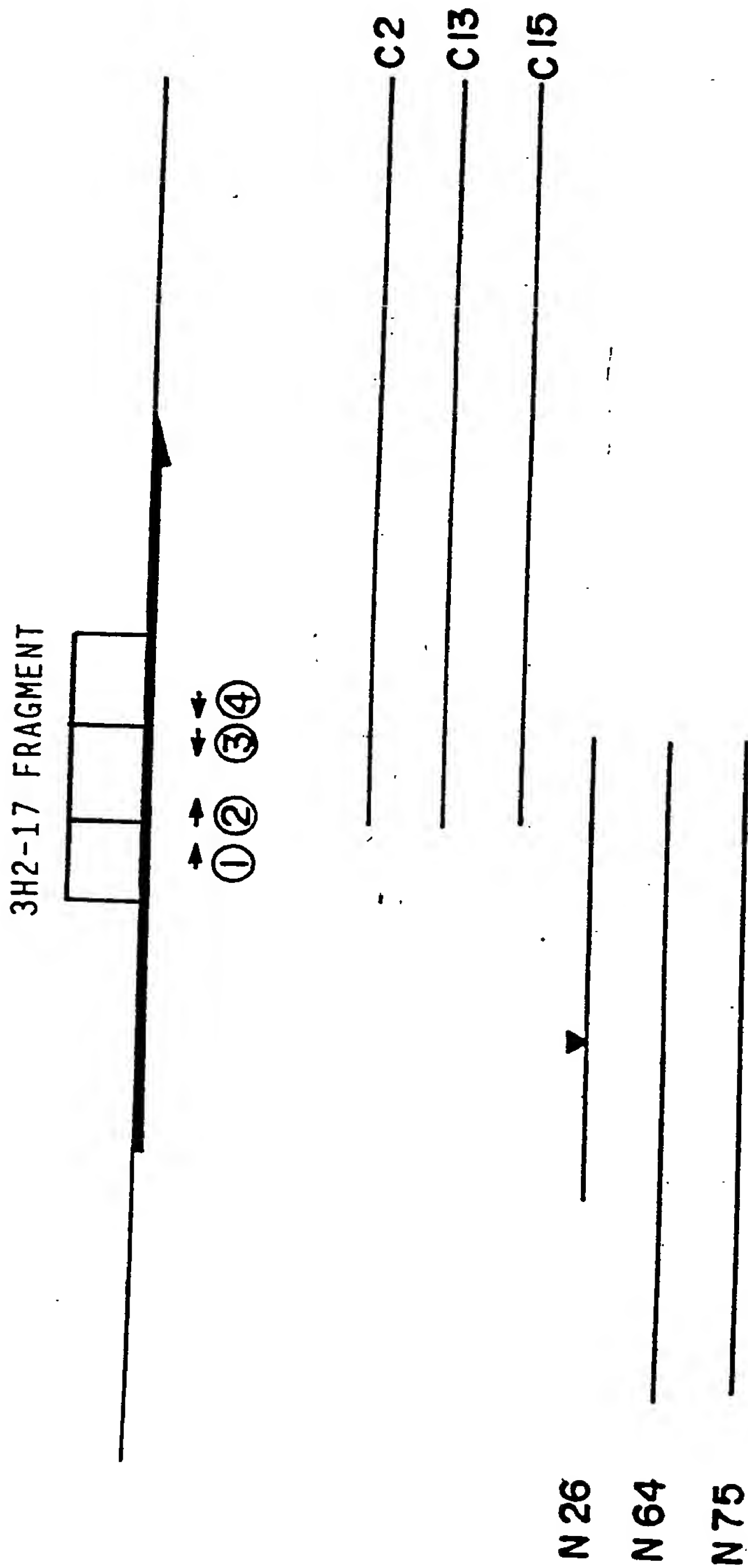
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FIGURE 67



10 9 8 7 6 5 4 3 2 1

FIGURE 68



C2 SPLEEN DERIVED C13 C15 THYMUS DERIVED
 N75 SPLEEN DERIVED N26 N64 THYMUS DERIVED
 ▼ PCR ERROR SITE

1	GAGCATAGGAAAGGCTGACAGGCAGTTATGGAGCAGGACAATGGCACCATCCAGGCTCCA	60
1	MetGluGlnAspAsnGlyThrIleGlnAlaPro	11
61	GGCTTGCCGCCCACCACCTGCGTCTACCGTGAGGATTTCAAGCGACTGCTGCTAACCCCG	120
11	GlyLeuProProThrThrCysValTyrArgGluAspPheLysArgLeuLeuLeuThrPro	31
121	GTATACTCGGTGGTGGCTGGTGGTGGCCTGCCACTGAACATCTGCGTCATTGCCCCAGATC	180
31	ValTyrSerValValLeuValValGlyLeuProLeuAsnIleCysValIleAlaGlnIle	51
181	TGCGCATCCCGCCGGACCCCTGACCCGTTCCGCTGTGTACACCCCTGAACCTGGCACTGGCG	240
51	CysAlaSerArgArgThrLeuThrArgSerAlaValTyrThrLeuAsnLeuAlaLeuAla	71
241	GACCTGATGTATGCCTGTTCACTACCCCTACTTATCTATAACTACGCCAGAGGGGACCAC	300
71	AspLeuMetTyrAlaCysSerLeuProLeuLeuIleTyrAsnTyrAlaArgGlyAspHis	91
301	TGGCCCTTCGGAGACCTCGCCTGCCGCTTTGTACGCTTCCTCTTCTATGCCAATCTACAT	360
91	TrpProPheGlyAspLeuAlaCysArgPheValArgPheLeuPheTyrAlaAsnLeuHis	111
361	GGCAGCATCCTGTTCCTCACCTGCATTAGCTTCCAGCGCTACCTGGGCATCTGCCACCCC	420
111	GlySerIleLeuPheLeuThrCysIleSerPheGlnArgTyrLeuGlyIleCysHisPro	131
421	CTGGCTTCCTGGCACAAGCGTGGAGGTGCGCGTGCTGCTTGGGTAGTGTGTGGAGTCGTG	480
131	LeuAlaSerTrpHisLysArgGlyGlyArgArgAlaAlaTrpValValCysGlyValVal	151
481	TGGCTGGCTGTGACAGCCCAGTGCCTGCCCACGGCAGTCTTTGCTGCCACAGGCATCCAG	540
151	TrpLeuAlaValThrAlaGlnCysLeuProThrAlaValPheAlaAlaThrGlyIleGln	171
541	CGCAACCGCACTGTGTGCTACGACCTGAGCCCCACCCATCCTGTCTACTCGCTACCTGCCC	600
171	ArgAsnArgThrValCysTyrAspLeuSerProProIleLeuSerThrArgTyrLeuPro	191
601	TATGGTATGGCCCTCACGGTCATCGGCTTCTTGCTGCCCTTCATAGCCTTACTGGCTTGT	660
191	TyrGlyMetAlaLeuThrValIleGlyPheLeuLeuProPheIleAlaLeuLeuAlaCys	211
661	TATTGTGCATGGCCCGCCGCTGTGTGCGCCAGGATGGCCCAGCAGGTCTGTGGCCCCAA	720
211	TyrCysArgMetAlaArgArgLeuCysArgGlnAspGlyProAlaGlyProValAlaGln	231
721	GAGCGGCGCAGCAAGGCGGCTCGTATGGCTGTGGTGGTGGCAGCTGTCTTTGCCATCAGC	780
231	GluArgArgSerLysAlaAlaArgMetAlaValValValAlaAlaValPheAlaIleSer	251
781	TTCTGCTTTCACATCACCACAGCCTACTTGGCTGTGCGCTCCACGCCCCGGTGTG	840
251	PheLeuProPheHisIleThrLysThrAlaTyrLeuAlaValArgSerThrProGlyVal	271
841	TCTTGCCCTGTGCTGGAGACCTTCGCTGCTGCCTACAAAGGCACTCGGCCCTTCGCCAGT	900
271	SerCysProValLeuGluThrPheAlaAlaAlaTyrLysGlyThrArgProPheAlaSer	291
901	GTCAACAGTGTCTTGACCCCATCTCTTCTACTTCACACAACAGAAGTTCCGGCGGCAA	960
291	ValAsnSerValLeuAspProIleLeuPheTyrPheThrGlnGlnLysPheArgArgGln	311
961	CCCCACGATCTCTTACAGAGGCTCACAGCCAAGTGCCAGAGGCAGAGAGTCTGAGGCCCC	1020
311	ProHisAspLeuLeuGlnArgLeuThrAlaLysTrpGlnArgGlnArgVal***	329

FIGURE 70

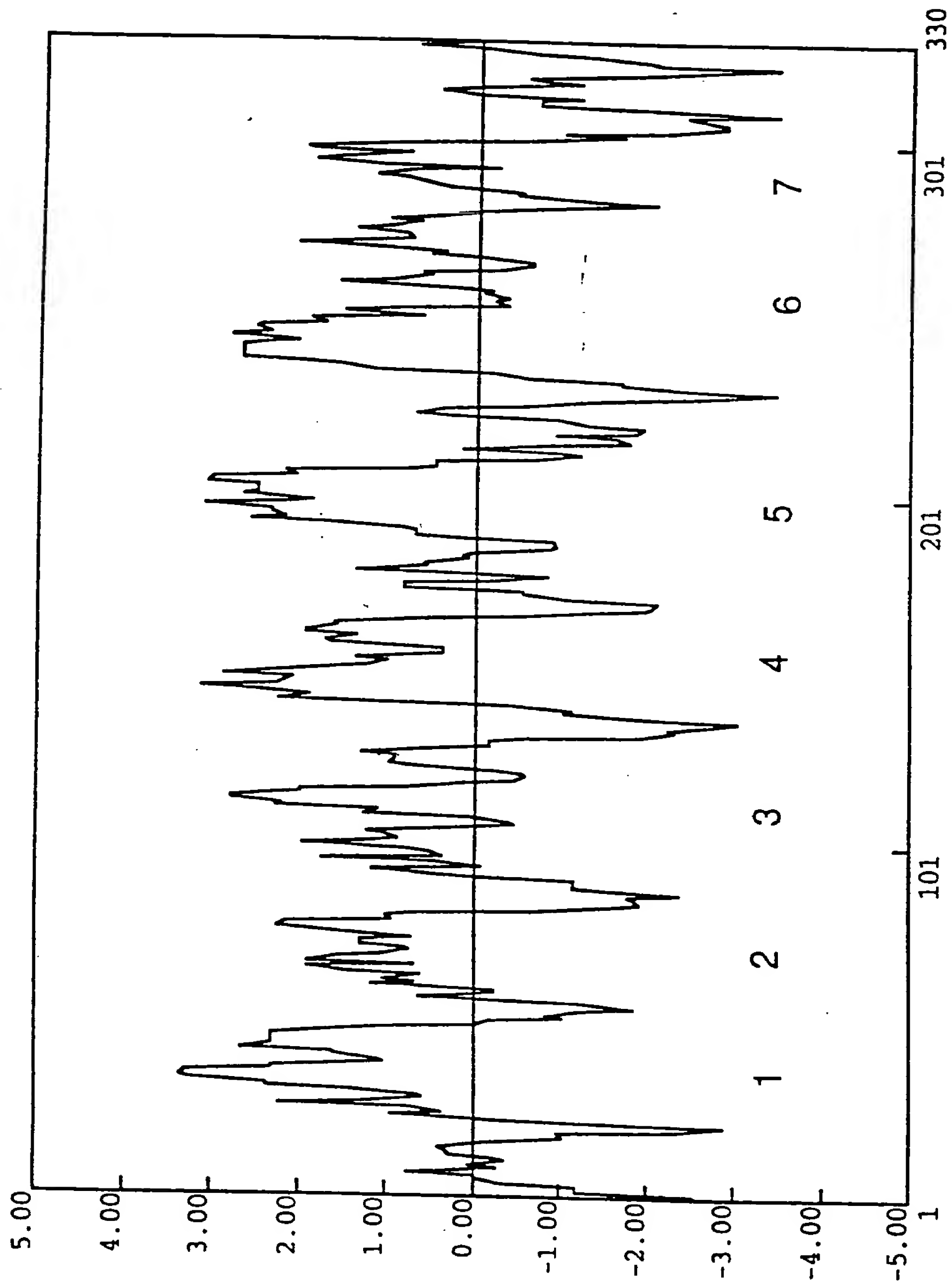


FIGURE 71

75+13, CODING	1	10	20	30	40	50	
P2UR_MOUSE	1	HEQD-----	--NGHIDAPG	PPP-----	-IM-SVYR-E	DEKRLILIP-	50
P2YR_CHICK	1	MAADLEPANS	TINGIWEQDE	LGY-----	---KCRFN-	DEKRVILIP-	50
	1	STEALISAAL	--NGHIDAPG	ELAGGWAAGN	ATWKCSLTXT	GEQFYVIL-ET	50
75+13, CODING	51	60	70	80	90	100	
P2UR_MOUSE	51	V-YSWVLVVG	-EPENICVIA	QH--CASRTI	LTR-SAVVIL	NLALADLMVA	100
P2YR_CHICK	51	VSYGWVCLG	-LCLNVVALY	-HFLC-RLKI	WNA-SITVME	HLEAVSDSYA	100
	51	V-YILVFTTS	FLG-NSVAIW	M-E-VFHMRP	WSGIS-VYME	NLALADFLV	100
75+13, CODING	101	110	120	130	140	150	
P2UR_MOUSE	101	CSLPILLIYV	ARG-DHWPEG	ELACRFVREF	FYANLHESIL	ELICISQORY	150
P2YR_CHICK	101	ASLPILLIYV	ARG-DHWPEG	TVLCKLVREF	FYANLHESIL	ELICISVHRC	150
	101	LTLPALLIYV	FNKTD-EIEG	DVMCKLQREF	SHVNLVGSIL	ELICISVHRY	150
75+13, CODING	151	160	170	180	190	200	
P2UR_MOUSE	151	EGICHPLASV	HKSGSE-SAA	WVCGVWVA	VTACCL-EIA	VEPA-IGIQE	200
P2YR_CHICK	151	EGVLRPLSL	--SWGRARYA	RRVAAVWV	VLA-CQAPV	YFVT-TSVRG	200
	151	TGWHPLKSL	G-SLKGQ-A	VYVSSLVWAL	WAVIA-PIL	-EYSGIGVRR	200
75+13, CODING	201	210	220	230	240	250	
P2UR_MOUSE	201	NRI-VGYDLS	PPI-E-SIRY	LPVGTALIV	GELLBEIALL	ACYCRMARRL	250
P2YR_CHICK	201	TE-ITICHDS	ARE-LFSHFV	A-YSSVMLGL	LEAVPFESVIL	VGYVLMARRL	250
	201	NKTHICVYIT	ADRYTSMEV	--YSHCTIVE	MSCIPEFVIL	GQYGLIVKAL	250
75+13, CODING	251	260	270	280	290	300	
P2UR_MOUSE	251	CROEGPA-GE	VACERRSKAA	--RMAVVVA	VEATSELEPH	IUKTAMLAVER	300
P2YR_CHICK	251	-LR--PAYGT	TGGLEPAKPK	SVETALVLA	VEALCETLEPH	VIRINLYSFR	300
	251	IYKD-LDNSP	---L-RRK--	SIYLVIIIVLT	VEAVSYLLEPH	VMKTNLNRAR	300
75+13, CODING	301	310	320	330	340	350	
P2UR_MOUSE	301	STP---GVSC	PVLETFAAAY	KGTRPFASVN	SVLDPIELVF	TOCKERRQPH	350
P2YR_CHICK	301	SLE----LSC	HTLNAINMAY	SIIRRELASAN	SCLDPIELVF	AGORLVRFAR	350
	301	-LDFQTPQMC	AFNDKVYATY	QVIRGLASLN	SCVDPIELVF	AGDTERRRLS	350
75+13, CODING	351	360	370	380	390	400	
P2UR_MOUSE	351	ELLQRLTAKW	QRORV*....	400
P2YR_CHICK	351	DAKPPTEPTP	SECARRKGL	HRPNRTVRKD	LSVSSDDSR	TESTPAGSET	400
	351	RATRKSRRS	EPNVQSKSEE	MTLNILLTEYK	QNGDTSL...	400
75+13, CODING	401	410	420	430	440	450	
P2UR_MOUSE	401	450
P2YR_CHICK	401	KDIRL.....	450
	401	450

FIGURE 72

5'	9			18			27			36			45			54		
	GCC	ACC	AAC	GTG	TTC	ATC	CTG	TCA	CTG	GCC	GAT	GTG	CTG	GTG	ACA	GCC	ATC	TGC
										---	---	---	---	---	---	---	---	---
										Ala	Asp	Val	Leu	Val	Thr	Ala	Ile	Cys
	63			72			81			90			99			108		
	CTG	CCG	GCC	AGT	CTG	CTG	GTA	GAC	ATC	ACG	GAA	TCC	TGG	CTC	TTT	GGC	CAT	GCC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Pro	Ala	Ser	Leu	Leu	Val	Asp	Ile	Thr	Glu	Ser	Trp	Leu	Phe	Gly	His	Ala
	117			126			135			144			153			162		
	CTC	TGC	AAG	GTC	ATC	CCC	TAT	CTA	CAG	GCC	GTG	TCC	GTG	TCA	GTG	GTC	GTG	CTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Cys	Lys	Val	Ile	Pro	Tyr	Leu	Gln	Ala	Val	Ser	Val	Ser	Val	Val	Val	Leu
	171			180			189			198			207			216		
	ACT	CTC	AGC	TCC	ATC	GCC	CTG	GAC	CGC	TGG	TAC	GCC	ATC	TGC	CAC	CCG	CTG	TTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Thr	Leu	Ser	Ser	Ile	Ala	Leu	Asp	Arg	Trp	Tyr	Ala	Ile	Cys	His	Pro	Leu	Leu
	225			234			243			252			261			270		
	TTC	AAG	AGC	ACT	GCC	CGG	CGC	GCC	CGC	GGC	TCC	ATC	CTC	GGC	ATC	TGG	GCG	GTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Phe	Lys	Ser	Thr	Ala	Arg	Arg	Ala	Arg	Gly	Ser	Ile	Leu	Gly	Ile	Trp	Ala	Val
	279			288			297			306			315			324		
	TCG	CTG	GCT	GTC	ATG	GTG	CCT	CAG	GCT	GCT	GTC	ATG	GAG	TGT	AGC	AGC	GTG	CTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Leu	Ala	Val	Met	Val	Pro	Gln	Ala	Ala	Val	Met	Glu	Cys	Ser	Ser	Val	Leu
	333			342			351			360			369			378		
	CCC	GAG	CTG	GCC	AAC	CGC	ACC	CGC	CTC	CTG	TCT	GTC	TGT	GAT	GAG	CGC	TGG	GCA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Pro	Glu	Leu	Ala	Asn	Arg	Thr	Arg	Leu	Leu	Ser	Val	Cys	Asp	Glu	Arg	Trp	Ala
	387			396			405			414			423			432		
	GAC	GAC	CTG	TAC	CCC	AAG	ATC	TAC	CAC	AGC	TGC	TTC	TTC	ATT	GTC	ACC	TAC	CTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Asp	Asp	Leu	Tyr	Pro	Lys	Ile	Tyr	His	Ser	Cys	Phe	Phe	Ile	Val	Thr	Tyr	Leu
	441			450			459			468			477			486		
	GCC	CCA	CTG	GGC	CTC	ATG	GCC	ATG	GCC	TAT	TTC	CAG	ATC	TTC	CGC	AAG	CTC	TGG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ala	Pro	Leu	Gly	Leu	Met	Ala	Met	Ala	Tyr	Phe	Gln	Ile	Phe	Arg	Lys	Leu	Trp
	495			504			513			522			531			540		
	GGC	CGC	CAG	ATC	CCC	GGC	ACC	ACC	TCG	GCC	CTG	GTG	CGC	AAC	TGG	AAG	CGG	CCC

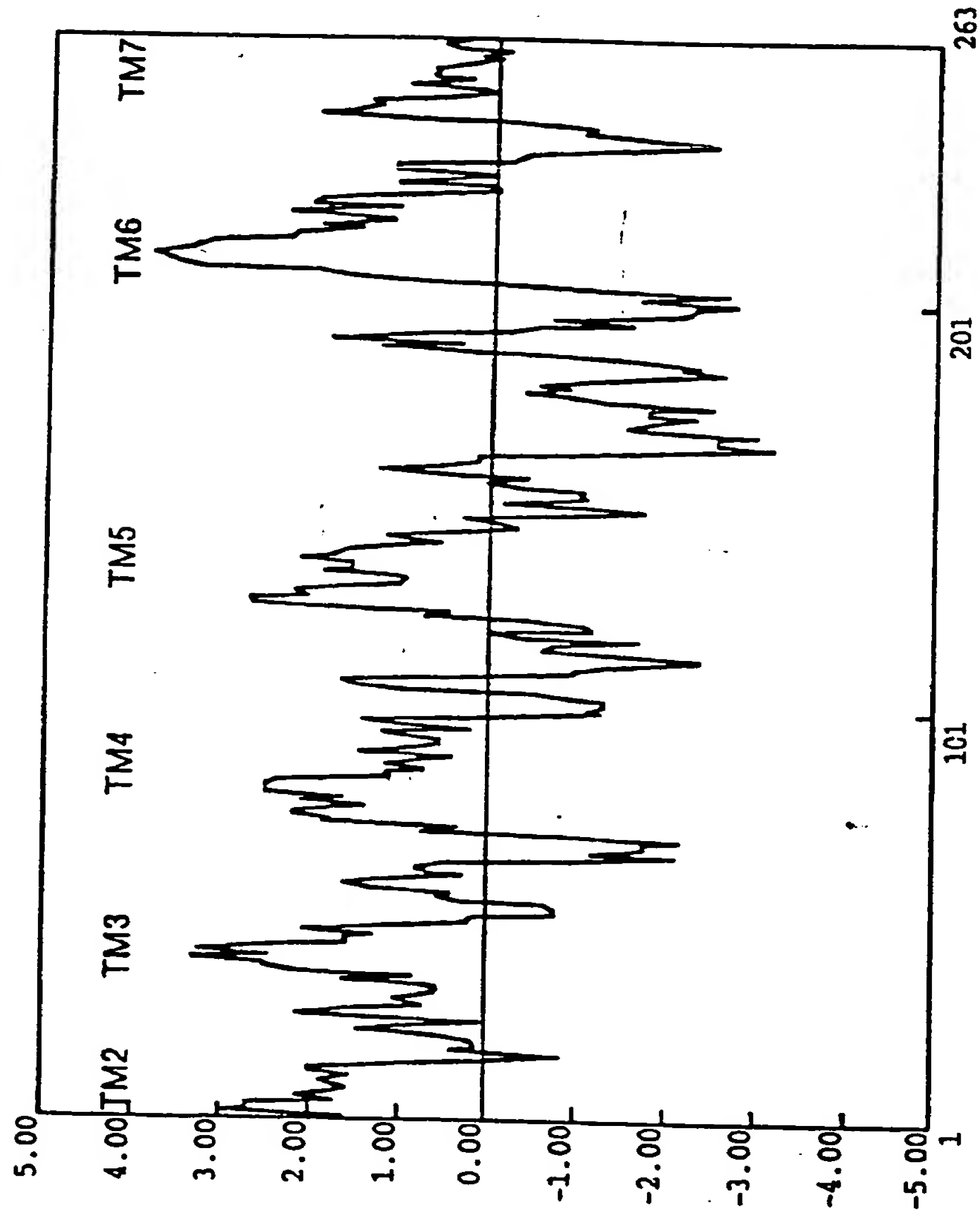
FIGURE 73

```

-----
Gly Arg Gln Ile Pro Gly Thr Thr Ser Ala Leu Val Arg Asn Trp Lys Arg Pro
      549      558      567      576      585      594
TCA GAC CAG CTG GAC GAC CAG GGC CAG GGC CTG AGC TCA GAG CCC CAG CCC CGG
-----
Ser Asp Gln Leu Asp Asp Gln Gly Gln Gly Leu Ser Ser Glu Pro Gln Pro Arg
      603      612      621      630      639      648
GCC CGC GCC TTC CTG GCC GAG GTG AAA CAG ATG CGA GCC CGG AGG AAG ACG GCC
-----
Ala Arg Ala Phe Leu Ala Glu Val Lys Gln Met Arg Ala Arg Arg Lys Thr Ala
      657      666      675      684      693      702
AAG ATG CTG ATG GTG GTG CTG CTG GTC TTC GCC CTC TGC TAC CTG CCC ATC AGT
-----
Lys Met Leu Met Val Val Leu Leu Val Phe Ala Leu Cys Tyr Leu Pro Ile Ser
      711      720      729      738      747      756
GTC CTC AAC GTC CTC AAG AGG GTC TTC GGG ATG TTC CGC CAA GCC AGC GAC CGA
-----
Val Leu Asn Val Leu Lys Arg Val Phe Gly Met Phe Arg Gln Ala Ser Asp Arg
      765      774      783      792      801      810
GAG GCC ATC TAC GCC TGC TTC ACC TTC TCC CAC TGG CTG GTG TAC GCC AAC AGC
-----
Glu Ala Ile Tyr Ala Cys Phe Thr Phe Ser His Trp Leu Val Tyr Ala Asn Ser
      819      828      837
GCC GCC AAT CCC CTC CTC TAC TCC TTC CTC CCT 3'
-----
Ala Ala

```

FIGURE 74



7 5 / 7 9

FIGURE 75

10 μ M ATP

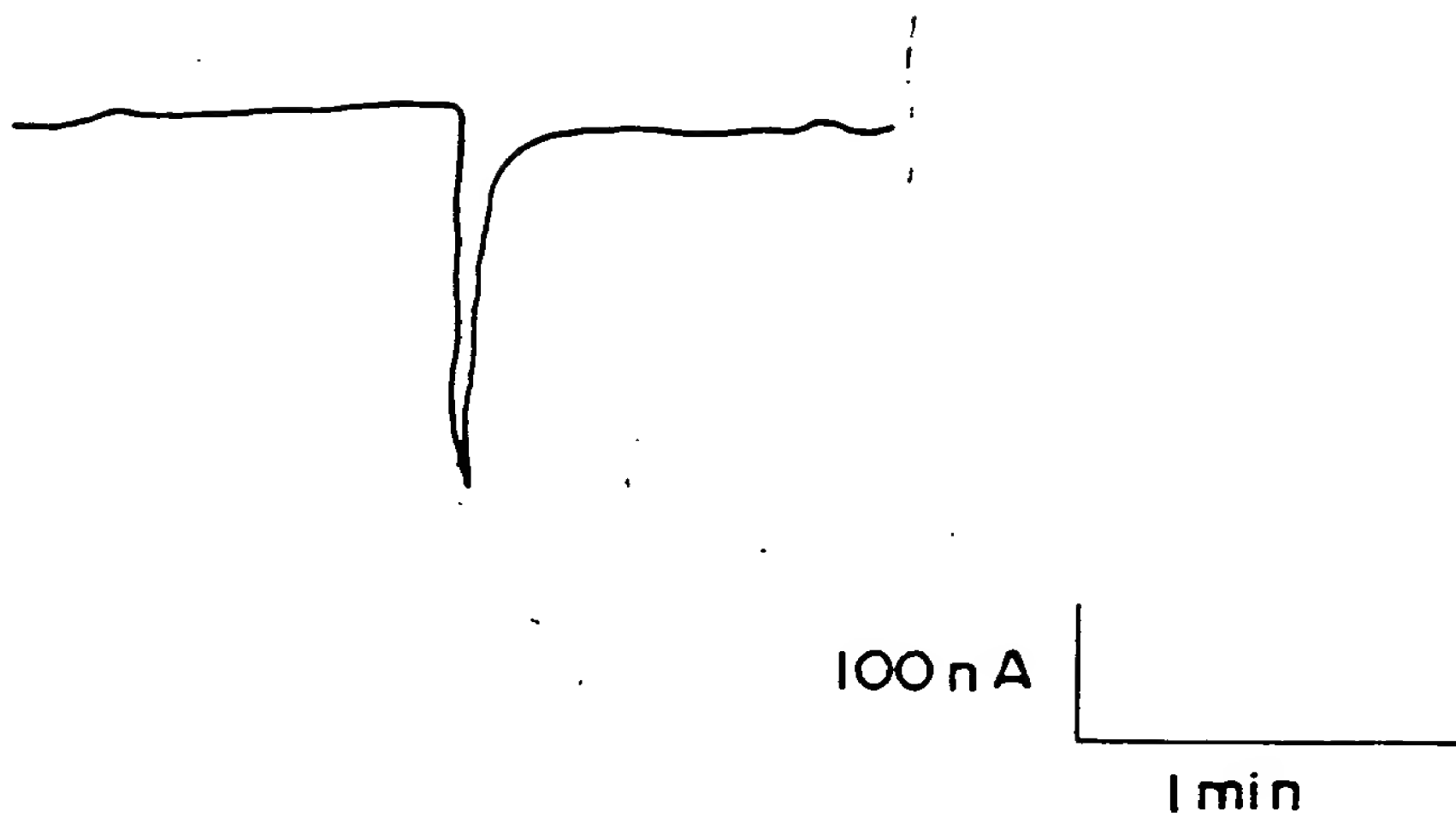


FIGURE 76

h3H2-17(5-3)	1	10	20	30	40	50	
p3H2-17(5')	1	GTGGGCTGG	TGGCAACAT	CTGGCTTCC	TGGACAAGC	GTGGAGTGC	50
							50
h3H2-17(5-3)	51	60	70	80	90	100	
p3H2-17(5')	51	CCGTGCTGCT	TGGTAGTGT	GTGGAGTGT	GTGGCTGGCT	GTGACAGCC	100
						GTGACAGCC	100
h3H2-17(5-3)	101	110	120	130	140	150	
p3H2-17(5')	101	AGTGGCTGG	CACAGCCATC	TTCCTGCCA	CAGCCTCCA	GCGTACCCG	150
	101	AGTGGCTGG	CAGGAGATC	TTCCTGCCA	CAGCCTCCA	GCGTACCCG	150
h3H2-17(5-3)	151	160	170	180	190	200	
p3H2-17(5')	151	ACTGCTGCT	ATGACCTCAG	CCGCTGTCG	CTGGCCACC	ACTATATGC	200
	151	ACTGCTGCT	ACGACCTGAG	CCGCTGTCG	CTGGCCACC	ACTATATGC	200
h3H2-17(5-3)	201	210	220	230	240	250	
p3H2-17(5')	201	CTATGCTATG	GCTCTACCTG	TGATGCGCT	CTTCCTGCG	TTTGCTGCC	250
	201	CTATGCTATG	GCTCTACCTG	TGATGCGCT	CTTCCTGCG	TTTGCTGCC	250
h3H2-17(5-3)	251	260	270	280	290	300	
p3H2-17(5')	251	AGTGGCTGG	CTACTGCTTC	CTGGCTGCG	GGG.....	300
	251	AGTGGCTGG	CTACTGCTTC	CTGGCTGCG	GGG.....	300
h3H2-17(5-3)	301	310	320	330	340	350	
p3H2-17(5')	301	CCAGCAGGTC	CTGTGGCCCA	AGAGCGGCG	AGCAAGGCG	CTCGTATGCG	350
	301	CCAGCAGGTC	CTGTGGCCCA	AGAGCGGCG	AGCAAGGCG	CTCGTATGCG	350
h3H2-17(5-3)	351	360	370	380	390	400	
p3H2-17(5')	351	TGTGGTGGTG	GCAGCTGTCT	TGCCCCCTG	CTGGCTGCC	CTCTAC....	400
	351	TGTGGTGGTG	GCAGCTGTCT	TGCCCCCTG	CTGGCTGCC	CTCTAC....	400

FIGURE 77

1	TGACTCCCTGAACATAGGAAACCCACCTGGGCAGCCATGGAATGGGACAATGGCACAGGC	60
1	MetGluTrpAspAsnGlyThrGly	8
61	CAGGCTCTGGGCTTGCCACCCACCACCTGTGTCTACCGCGAGAACTTCAAGCAACTGCTG	120
8	GlnAlaLeuGlyLeuProProThrThrCysValTyrArgGluAsnPheLysGlnLeuLeu	28
121	CTGCCACCTGTGTATTCGGCGGTGCTGGCGGCTGGCCTGCCGCTGAACATCTGTGTCATT	180
28	LeuProProValTyrSerAlaValLeuAlaAlaGlyLeuProLeuAsnIleCysValIle	48
181	ACCCAGATCTGCACGTCCCGCGGGCCCTGACCCGCACGGCCGTGTACACCCTAAACCTT	240
48	ThrGlnIleCysThrSerArgArgAlaLeuThrArgThrAlaValTyrThrLeuAsnLeu	68
241	GCTCTGGCTGACCTGCTATATGCCTGCTCCCTGCCCCCTGCTCATCTACAACCTATGCCCAA	300
68	AlaLeuAlaAspLeuLeuTyrAlaCysSerLeuProLeuLeuIleTyrAsnTyrAlaGln	88
301	GGTGATCACTGGCCCTTTGGCGACTTCGCCTGCCGCTGGTCCGCTTCCTCTTCTATGCC	360
88	GlyAspHisTrpProPheGlyAspPheAlaCysArgLeuValArgPheLeuPheTyrAla	108
361	AACCTGCACGGCAGCATCCTCTTCTCACCTGCATCAGCTTCCAGCGCTACCTGGGCATC	420
108	AsnLeuHisGlySerIleLeuPheLeuThrCysIleSerPheGlnArgTyrLeuGlyIle	128
421	TGCCACCCGCTGGCCCCCTGGCACAACGTGGGGGGCCGGGGCTGCCTGGCTAGTGTGT	480
128	CysHisProLeuAlaProTrpHisLysArgGlyGlyArgArgAlaAlaTrpLeuValCys	148
481	GTAACCGTGTGGCTGGCCGTGACAACCCAGTGCCCTGCCACAGCCATCTTCGCTGCCACA	540
148	ValThrValTrpLeuAlaValThrThrGlnCysLeuProThrAlaIlePheAlaAlaThr	168
541	GGCATCCAGCGTAACCGCACTGTCTGCTATGACCTCAGCCCGCCTGCCCTGGCCACCCAC	600
168	GlyIleGlnArgAsnArgThrValCysTyrAspLeuSerProProAlaLeuAlaThrHis	188
601	TATATGCCCTATGGCATGGCTCTCACTGTATCGGCTTCCTGCTGCCCTTTGCTGCCCTG	660
188	TyrMetProTyrGlyMetAlaLeuThrValIleGlyPheLeuLeuProPheAlaAlaLeu	208
661	CTGGCCTGCTACTGTCTCCTGGCCTGCCGCTGTGCCGCCAGGATGGCCCGGCAGAGCCT	720
208	LeuAlaCysTyrCysLeuLeuAlaCysArgLeuCysArgGlnAspGlyProAlaGluPro	228
721	GTGGCCCAGGAGCGGCGTGGCAAGGCGGCCCGCATGGCCGTGGTGGTGGCTGCTGCCTTT	780
228	ValAlaGlnGluArgArgGlyLysAlaAlaArgMetAlaValValValAlaAlaAlaPhe	248
781	GCCATCAGCTTCCTGCCTTTTTCACATCACCAAGACAGCCTACCTGGCAGTGGGCTCGACG	840
248	AlaIleSerPheLeuProPheHisIleThrLysThrAlaTyrLeuAlaValGlySerThr	268
841	CCGGGCGTCCCCTGCACTGTATTGGAGGCCTTTGCAGCGGCCTACAAAGGCACGCGGCCG	900
268	ProGlyValProCysThrValLeuGluAlaPheAlaAlaAlaTyrLysGlyThrArgPro	288
901	TTTGCCAGTGCCAAACAGCGTGCTGGACCCCATCCTCTTCTACTTCACCCAGAAGAAGTTC	960
288	PheAlaSerAlaAsnSerValLeuAspProIleLeuPheTyrPheThrGlnLysLysPhe	308
961	CGCCGGCGACCACATGAGCTCCTACAGAAACTCACAGCCAAATGGCAGAGGCAGGGTCGC	1020
308	ArgArgArgProHisGluLeuLeuGlnLysLeuThrAlaLysTrpGlnArgGlnGlyArg	328
1021	TGA	1023
328	***	329

FIGURE 78

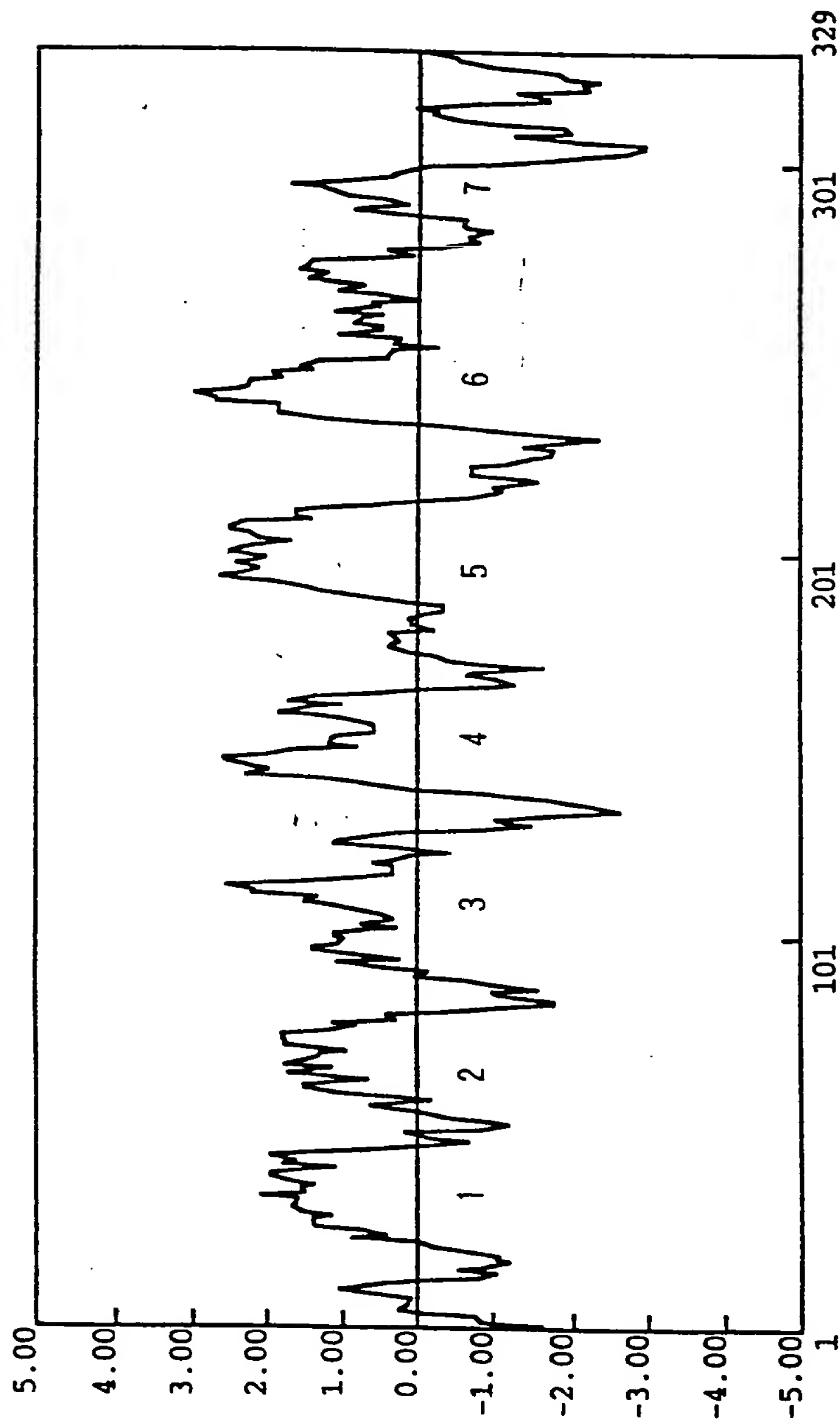


FIGURE 79

human prino, mouseFULL3H2	1	10	20	30	40	50
	1	MEWDNGTQQA	LGLPPTTCVY	RENEKQLLLP	PVYSVLAAG	LPLNICVING
	1	MEQDNGTIOA	PGLPPTTCVY	REDEKRLLLT	PVYSVLAAG	LPLNICVING
human prino, mouseFULL3H2	51	60	70	80	90	100
	51	ICTSRRALTR	TAVYTNLAL	ADLYACSLP	LLIYNVADGD	HWPFQDFACR
	51	ICASRRFLTR	SAVYTNLAL	ADLYACSLP	LLIYNVADGD	HWPFQDFACR
human prino, mouseFULL3H2	101	110	120	130	140	150
	101	LVRFLFYANL	HGSILFLTCT	SFQRYLGICH	PLAPWHKRGG	RRAAWLVCVT
	101	FVRFLFYANL	HGSILFLTCT	SFQRYLGICH	PLAPWHKRGG	RRAAWLVCVT
human prino, mouseFULL3H2	151	160	170	180	190	200
	151	VMLAVTQOCL	PTAIFAATGI	QRNRTVCYDL	SPPALATHYM	PYGNALTVIG
	151	VMLAVTQOCL	PTAIFAATGI	QRNRTVCYDL	SPPALATHYM	PYGNALTVIG
human prino, mouseFULL3H2	201	210	220	230	240	250
	201	ELLPEAALLA	CYCLLACRLC	RODGPAPVPA	QERRSKAARM	AVVVAAPFAI
	201	ELLPEAALLA	CYCLLACRLC	RODGPAPVPA	QERRSKAARM	AVVVAAPFAI
human prino, mouseFULL3H2	251	260	270	280	290	300
	251	SFLPEHITKT	AYLAVGSTPG	MPCLVLEAFA	AAYKGTTRPFA	SAANSVLDPIL
	251	SFLPEHITKT	AYLAVGSTPG	MPCLVLEAFA	AAYKGTTRPFA	SAANSVLDPIL
human prino, mouseFULL3H2	301	310	320	330	340	350
	301	FYFTQCKFRR	RPHLLQKLT	AKWQRQR*
	301	FYFTQCKFRR	RPHLLQKLT	AKWQRQR*